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MPsrch\_pp Run on: protein - protein database search, using Smith-Waterman algorithm Tue Sep 26 16:16:03 2000; MasPar time 9.87 Seconds 731.891 Million cell updates/sec

Tabular output not generated

Title:

Description: Perfect Score: >US-09-308-435-2 (28-260) from US09308435.pep 1594

Sequence: 1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45

summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 48.589; Variance 103.194; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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HISTIDINE BIOSYNTHESIS	PHOSPHOGLYCERATE KINAS	PEPTIDYL-TRNA HYDROLAS	HAP3 TRANSCRIPTIONAL A	SPECTRIN ALPHA CHAIN.	HYPOTHETICAL PROTEIN M	DIHYDROPYRIDINE-SENSIT	ALVEOLYSIN PRECURSOR (	ADENYLOSUCCINATE SYNTH	ACIDIC RIBOSOMAL PROTE	ENDONUCLEASE G PRECURS	PHOSPHATIDYLINOSITOL 3	-REPAIR	104.	LIPOXYGENASE (EC 1.13.	SYNAPTONEMAL COMPLEX P	2,4-DIENOYL-COA REDUCT	PUTATIVE 49.7 KDA MEMB	O-ANTIGEN LIGASE.	KERATIN, TYPE I CYTOSK	COATOMER EPSILON SUBUN
1.67e+01 1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.31e+01	1.31e+01	1.31e+01	1.31e+01	1.31e+01	1.31e+01	1.31e+01	1.02e+01	1.02e+01	1.02e+01	7.94e+00	1.02e+01	7.94e+00	1.02e+01	1.02e+01	7.94e+00	1.02e+01

## ALIGNMENTS

RESULT ID H AC Q	1 PA3_HELPY 48261; 1-NOV-1997	STANDARD;	PRT;	260 AA.	PA.
i i	01-NOV-1997 (	01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation undate)	quence	updat	e)
DE	NEURAMINYLLAC	NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-	GGLUT	ININ P	RECURSOR (N-
DH	ACETYLNEURAMI	NYLLACTOSE-BINDIN	(G FIB	RILLAR	ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-
DE	BINDING SUBUN	BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN).	ELLAR :	SHEATH	ADHESIN).
G R	HPAA.				
တ္ထ	Helicobacter	Helicobacter pylori (Campylobacter pylori).	icter 1	pylori	•
გ	Bacteria; Pro	oteobacteria; epsi	lon si	ipdivi	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group:
გ	Helicobacter.				9-047
RN	[1]				
RP	SEQUENCE FROM N.A.	N.A.			
RC	STRAIN-NCTC 11637;	1637;			
쫎	MEDLINE; 97431527.	1527.			
RA	Jones A.C., L	ogan R.P., Foynes		Cockayı	Jones A.C., Logan R.P., Foynes S., Cockayne A., Wren B.W., Penn C.W.:
RT	"A flagellar	sheath protein of	Heli	cobacte	"A flagellar sheath protein of Helicobacter pylori is identical to
RT	HpaA, a putat	ive N-acetylneura	minyli	lactose	HpaA, a putative N-acetylneuraminyllactose-binding hemagglutinin, but
RT	is not an adh	is not an adhesin for AGS cells.";			
꺕	J. Bacteriol.	Bacteriol. 179:5643-5647(1997).	97).		
റ്റ	-1- SUBCELLUL	AR LOCATION: ATTA	CHED	THE	-1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIDID
ဂ	ANCHOR (P	ANCHOR (PROBABLE).			
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 233; Conservative This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Score 1594; DB 1; 1 Pred. No. 1.03e-279; 0; Mismatches 0;

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Flagella;
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                                                                                                                                                                                                                                                                                                                                          pylori.";
Nature 388:539-547(1997).
-i- SUBCELLULAR LOCATION: ATTACHED
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-
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MEDLINE; 97394467.
                                                                                                          SEQUENCE
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                                                                  Similarity
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larity 98.7%;
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Pred. No. 6.:
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTINN PRECURSOR
ACETYLMEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLU
BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN)
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PROSITE; PS00013; PROKAR_LII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The putative neuraminyllactose-binding hemagglu: Helicobacter pylori CCUG 17874 is a lipoprotein. J. Bacteriol. 177:6049-6057(1995).
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O'Toole P.W.,
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embrane; Lipoprotein; Signal.
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BY SIMILARITY.
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Pred.
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N-ACYL DIGLYCERIDE (PROBABLE).

N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).

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SHEATH ADHESIN).
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans D.G., Karjalainen T.K., Evans D.J., Graham I "Cloning, nucleotide sequence, and expression of adhesin subunit protein of Helicobacter pylori."; J. Bacteriol. 175:674-683(1993).

-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter
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01-NOV-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-
ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ
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Q48264;
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larity 95.7%;
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embrane; Lipoprotein; Signal.
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260 NEURAMINYLLACTOSE-BINDING
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Pred. No. 3.53e-271;
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N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
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SEQUENCE
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NON_TER
SEQUENCE FROM N.A.
MEDLINE; 96001251.
Evans D.G., Lampert H.C.,
Bronsdon M.A., Evans D.J.
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-I- SUBCELLULAR LOCATION:
ANCHOR (PROBABLE).
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Evans D.G., Lampert H.C., Nakano
Bronsdon M.A., Evans D.J. Jr.;
"Genetic evidence for host specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPAA OR HNAA.
Helicobacter nemestrinae.
Bacteria; Proteobacteria;
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
                                                                                                                              Helicobacter acinonyx.
Bacteria; Proteobacteria;
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TE; PS00013; PROKAR_I
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SEQUENCE
                                                                                                                                                                                                                                                           Bell S.P., Mitchell J., Leber J., Kobayashi R., 8 "The multidomain structure of Orclp reveals simil of DNA replication and transcriptional silencing Cell 83:563-568(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ORIGIN RECOGNITION COMPLEX SUBUNIT 3 (ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORC3_YEAST P54790;
                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96239540. Hardy C.F.J.;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MEDLINE; 96069857.
                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN 62 KDA SUBUNIT).
ORC3 OR OAF1 OR OIF1 OR YLL004W OR L1365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetaceae;
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Yeast 12:693-708(1996).
'I FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC)
BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSY
REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS
THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.
'I SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS OF 120 KDA, 71 KDA
KDA, 56 KDA, 53 KDA AND 50 KDA.
                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 29342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; L0003074; ORC3.

DNA replication; Nuclear protein; DNA-binding.
SEQUENCE 616 AA; 72077 MW; 3FAAEE3F645D3F9C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U34861; AAB38249.1; --
EMBL; U48888; AAC49270.1; --
EMBL; X91488; CAA62765.1; --
EMBL; Z73109; CAA97447.1; --
SGD; L0003074; ORC3.
                                                                                                                                                                                pneumoniae.
                                                                                                                                                                                                                          Herrmann R.
                                                                                                                                                                                                                                           Himmelreich R.,
                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacill
Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYFB_MYCPN
                                                                                                                                                                                                 Complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7 kb fragment of chromosome XII including an open omologous to the human cystic fibrosis transmembrane
                                                          (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                               PYROPHOSPHATE + L-
SUBUNIT: TETRAMER
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LQNQGYKVISYDSSDKDDFSFAQKK-EGYLAVAMNGEIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLLKRNYHKLDV-SSNKG-FKYGNQIFQSFLD-TVDGKLNL
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26; Conser
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                                                                                                                                                                                                                                                                  97105885
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larity 25.7%;
Conservative
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                                                                                                                                                                                                                                         Hilbert H.,
                                                                                                                                                                                                     analysis
                                                                                                                                                                                                                                                                                     M129;
                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium
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Pred.
33; M
                                                                                                                                                                                                     of.
                                                                                                                                                                                                                                         Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             re 107; DB 1; I
d. No. 4.42e-01;
Mismatches 32;
                                                                                                                                                                                                     genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      805
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There are no restrictions
ng as its content is in
                                                                                                                                                                                                                                         Pirkl E.,
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                                                                                                  BETA
                                                                                                                                                                                                                                                                                                                                                                 group;
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                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129
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                                                                                                                                                                                                 bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                               .20) (PHENYLALANINE--
                                                                                                                                                                                                                                           Li B.-C
                                                                                                                                                                                                                                                                                                                                                                 Mollicutes;
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E CHROMOSOMAL
ING. BINDS TO
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a collaboration -
MBL outstation -
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Best Local S
Matches 2
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Best Local Similarity
Matches 21; Conser
  MTNX_NEILA
P24581;
01-MAR-1992
01-MAR-1992
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YJI3_YEAST STANDARD; PRT; 18U3 AA. PA7024; P87192; 01-FEB-1996 (Rel. 33, Created) 15-FEB-2000 (Rel. 39, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) TRANSPOSON TY4 207.7 KDA HYPOTHETICAL PROTEIN. TY4B OR YJL113W OR J0780.
                                                                                                                                              1231
                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                        1171
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.; "Sequencing analysis of a 40.2 kb fragment of yeast chromosome X "reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2 SPT10, GCD14, REE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon."; Yeast 12:1471-1474(1996).
                                                                                                                                                                                                                                                                                           Transposable SEQUENCE 18
                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       EMBL; Z49389; CAA89409.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C / FY1679;
MEDLINE; 97103775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aminoacyl-tRNA synthetase; SEQUENCE 805 AA; 91713 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000006; AAB95696.1;
                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565
                                                                                                                                              DKNNSLTSYELERDKKRSKKNR 1252
                                                                                                                                                                        DISELDIQEKFIKTTHSSHSGGIVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                                                                      NLKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                   TQKN-LESYQKDAKELKGKRNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 6.6%;
Similarity 28.4%;
23; Conservative
                                                                                                                                                                                                                                                                                        le element; Hypothetical protein.
1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;
 (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 36, Last annotation updat
                                                                                                                                                                                                                                  Conservative
                                                           STANDARD;
                                                                                                                                                                                                                                              25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584
                                                                                                                   260
                                                                                                                                                                                                                                 Score 105; DB 1;
Pred. No. 7.61e-01
28; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 1; Le
Pred. No. 7.61e-01;
21; Mismatches 33;
                                                         313
 update)
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                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                           Length 1803
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                                                                                                                                                                                                                                 Indels
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                                                      SEQUENCE FROM N.A.
STRAIN-NRRL Y-1094;
MEDLINE, 92380493.
*Strick C.A., James L.C., O'Donnell M.M.,
"The isolation and characterization of tyene from the yeast Yarrowia lipolytica.
Gene 118:65-72(1992).
                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PYRUVATE KINASE (EC 2.7.1.40).
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycolipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                         KPYK_YARLI
P30614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0105; C5METTRFRASE.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED CCNGG, CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANI-I-CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOS: S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of two ta
methyltransferase genes of Neisseria
M.NIaIII and a cytosine-type methylase.
Mol. Gen. Genet. 224:101-110(1990).
MEDLINE; 94171073.
Strick C.A., James
                             ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Methyltransferase; Restriction system.
ACT_SITE 74 74 BY SIMILARITY.
SEQUENCE 313 AA; 34842 MW; E75150C89ABEA611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54485; CAA38357.1; PIR; S12037; XYNHCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOSINE-SPECIFIC METHYLTRANSFERASE NLAX (EC 2.1.1.73) (M.NLAX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REBASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria
                                                                                                                                                                                                                                                                                                                                                113
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                                                                                                                                                                                                                                                                                                                                                                                                     QKKEG-YLAVAMNGEIVLR-PDP
                                                                                                                                                                                                                                                                                                                                                                         QNRERIYLVGFLNHDVDFRFPQP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E; RB02158; M.Nlax.
PF00145; DNA_methylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 6.5%;
Similarity 34.9%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoeltke H.J.,
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  James
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                                                                                                                                                                                                                                                                                      STANDARD;
 r.c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lau P.C.
  O'Donnell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104; DB 1; Lu
Pred. No. 9.95e-01;
18; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                133
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                                                                                                                                                                                      Saccharomycetes;
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 M.M.,
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 Gollaher
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                                                                                                 Gollaher
                                                                                ollaher M.
pyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 313;
                                                                                                                                                                                      Saccharomycetales;
 м.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                 .G., Franke A.E., kinase-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOSINE
 Franke
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 A.E.,
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Query Match
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Q57775;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                      This SWI
between
the Euro
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                                                                                                        Science 273:1058-1073(1996).
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COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.

COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM.

PATHWAY: FINAL STEP IN GLYCOLYSIS.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
                      European
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                                     SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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Similarity 23.1%;
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and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
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se; Glycolysis; Magnesium.
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pFAM; pF000509; pkinase; 1.
pFAM; pF00433; pkinase_C; 1.
pROSITE; pS001007; pROTEIN_KINASE_ATP; 1.
pROSITE; pS00101; pROTEIN_KINASE_DOM; 1.
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pROSITE; pS500179; DAG_PE_BINDING_DOMAIN; 2.
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O84533;
01-OCT 1996 (Rel. 34, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTE:
TRNA LIGASE) (CYSRS).
TRNA LIGASE) (CYSRS).
TRNA LIGASE) (CYSRS).
SACCharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 99000809.
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis. Bacteria; Chlamydiales;
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                                                                                                                               YNY7_YEAST
P53852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of an obligate intracellular pathogen of
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15-FEB-2000 (Rel.
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Similarity 36.7%;
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Pred. No. 2.86e+00;
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13; Mismatches
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Best Local Similarity 27.7%;
Matches 18; Conservative
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EMBL; Z71523; CAA96154.1; -.
PFAM; PF01406; tRNA-synt_1e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poehlmann R., Philippsen P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ATP + L-CYSTEINE + TRNA(CYS) = AMP +
-YRODHOSPHATE + L-CYSTEINYL-TRNA(CYS).
-i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                    SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97377992.
                                                                                                                                                                                                                                   PRINTS; PR00983; TRNASYNTHCYS.

PROSTIE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

Hypothetical protein; Aminoacyl-trNA synthetase; Protein biosynthesis;

Ligase; ATP-binding.

SIMILAR
5 75 "HIGH" REGION.

SIMILAR 427 431 "KMSKS" REGION.

BINDING 430 430 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hegemann J.H.;
"Sequence analysis of the 33 kb long region between ORC5 and SUI1.
"From the left arm of chromosome XIV from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler
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                                    160 TIEEF 164
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   DKDDF 109
                                                                        EKVQALDEKILL-LRPAFQYSDNIAKEYENKFKNQTALKVEQIL-Q--NQGYKVISVDSS 104
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430
767 AA;
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Pred. No. 2.20e+00;
16; Mismatches 26;
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ATP (BY SIMILARITY).
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Search completed: Tue Sep 26 16:16:16 2000 Job time : 13 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

.Psrch\_pp protein - protein database search, using Smith-Waterman algorithm Tue Sep 26 16:18:57 2000; MasPar time 8.99 Seconds 613.770 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-09-308-435-4
(28-260) from US09308435.pep
1599
1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 32.470; Variance 175.985; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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302 302 235 235 227 176 118 109 100 100 103 103 103	1599 1599 1589 1589 1589 1547 1547	Score
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H. Pylori derived prot H. Pylori derived prot H. Pylori ORF 0lae1101 H. Pylori ORF 0615 pr H. Pylori GRPO 1615 pr H. Pylori GRPO 4621100 H. Pylori secreted or H. Pylori secreted or Grapevine leafroil vir ORC3 subunit of yeast S. cerevisiae origin o Haemophilus paragallin Haemophilus paragallin Merozite apical-end-lo Merozoite apical-end-lo	ter pylo ter pylo ter pylo ter pylo ter pylo (,cholera (	Description
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ein sequ	XAP-1, part of the DNA	Human neuronal calcium	calci	94 p	_	Grapevine leafroll vir	Borrelia VS461 antigen	d pyruvat	Recombinant cold-resis	Petunia MADS box trans	Spinocerebellar ataxia		Spinocerebellar ataxia	Human heart muscle spe	Amino acid sequence of	Completely humanised C	1 sequenc		Fragment of humanised	Humanised C4G1 Ig heav	Amino acid sequence of
	8.57e+01					8.57e+01			7.48e+01	7.48e+01	6.53e+01	(л	6.53e+01	UI		Ġ		ċn	6.53e+01	6.53e+01	6.53e+01

# ALIGNMENTS

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This polypeptide comprises a 29 kDa surface antigen which is comprises on the dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is an adhesin that is conserved in all tested strains of H. pylori, and is also a putative virulence factor. The invention relates to a new pharmaceutical composition comprising a lipid aggregate of a new pharmaceutical composition comprising a lipid aggregate of a negatively charged lipid or lipid mixture and at least one cantigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see V34643) coding for such an antigen. The new formulations, which are useful as vaccine formulations, elicit a protective immune response against H. pylori infections, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second, claimed 29 kDa antigen (see W60156) is provided that differs only at residue 222 (Ser for Arg).
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Best Local S
Matches 23
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18-NOV-1997; SE1927.
22-NOV-1996; SE-004296.
(ASTR ) ASTRA AB.
Berglindh T, Lofroth J;
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Helicobacter pylori 29 kDa surface-exposed antigen.
Cell surface antigen; adhesin; infection; vaccine; Helicobacter pylori.
W09822135-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aggregate of negatively charged lipid and Helicobacter pylori antigen - useful in therapeutic or preventative vaccines against both forms of bacterium, to generate systemic and mucosal antibody
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                                                                                     STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Similarity 100.0%; 233; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Score 1599; DB 1;
Pred. No. 2.57e-113;
0; Mismatches 0;
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Best Local 9
                                                                                           Antigen; adhe;
therapy; diag;
Helicobacter;
                                                                                                                                                                                    W07449 stand
W07449;
04-MAR-1997
cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylactic use. An adequate response is produced even wided adjuvant. A second 29 kDa antigen (see W60157) is provided differs only at residue 222 (Arg for Ser).
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Aggregate of negatively charged lipid and Helicobacter pyloriantigen - useful in therapeutic or preventative vaccines again both forms of bacterium, to generate systemic and mucosal ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1998 (first entry) Helicobacter pylori 29 kDa surface-exposed antigen. Cell surface antigen; adhesin; infection; vaccine; drug delivery. Helicobacter pylori.
                                                                                                                                                            Helicobacter pylori
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22-NOV-1996; SE-004296.
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                                                                                                                                                                                                                               standard; Protein; 260
                                      diagnosis.
diagnosis.
cter pylori strain CCUG 17874 (NTCC Location/Qualifiers
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Similarity 99.6%;
                                                                                                                                    adhesin; immunogen;
                                                                                                                                                                                    (first entry)
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/label= Sig_peptide
25. .28
                                                                                                                                                              surface-exposed
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Pred. No. 1.
0; Mismatc
                                                                                                                                      vaccine;
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                                                                                                                                                              29
                                                                                                                                 kDa antigen.
immunisation;
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Claim 2; Page 34-35; 49pp; English.

Claim 2; Page 34-35; 49pp; English.

Claim 2; Page 34-35; 49pp; English and dividing forms of the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43835) differs only at position 222 (Arg for Ser). Recombinant cantigen can be produced in transfer dost cells. It is useful for the diagnosis and treatment of H. pylori infections and for use as a vaccine.
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Best Local :
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21-MAY-1997; 000091.
21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO L
(Kim BO, Lee BK, Park SK, Yo
Fusion gene consisting of the Helicobacter pylori adhesin gene ligated to the A2 and B subunit gene of Vibrio cholerae toxin useful in the diagnosis and treatment of H. pylori Claim 2; Page 20-21; 32pp; English.
                                                                                                                                WPI; 98-434925/37.
N-PSDB; X21955.
                                                                                                                                                                                                                                                                                                                                                                                                duodenal ulcer.
Chimeric - Helicobacter pylori.
Chimeric - Vibrio cholerae.
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Bolin I, Svennerholm A;
WPI; 97-034307/03.
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Adhesin/V.chol
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05-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit; B subunit;
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SE-001085.
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larity 99.6%;
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i infection;
diagnosis;
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adhesin gene; V. cholerae
vaccine; gastritis; gastri
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.58e-112;
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H. pylori adhesin gene, and the V. cholerae toxin A2 and B subunit genes. CC This protein is used in the diagnosis of and as a vaccine against CC H. pylori, which is the main cause of gastritis and gastric/duodenal CC ulcers. It may also be used in the production of an anti-H. pylori CC antibody. Vectors containing the DNA sequence and E. coli strains CC containing it form the basis of a process to produce the protein, which CC consists of culturing the microorganism and obtaining the protein. The CC protein is an effective vaccine against H. pylori due to its excellent CC and its ability to penetrate through the stomach environment, CC stimulate sigh production.

CC Note: This sequence was indexed from W09853082, which is the first CC major country equivalent to KR97059278.
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Best Local S
Matches 23
                                                                                                                                                                                                  Smith D;
...r; 98-271811/24.
N-PSDB; X30467.
Helicobacter -
reduct-
                                                                                                                                                                                                                                                                                          07-MAY-1998.
28-OCT-1997; U19575.
14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
         Recombinant or substantially pure preparations of H. pylori polypepti are disclosed, together with the nucleic acids encoding them. In all, 73 ORFS are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at less nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; probe; d secreted protein;
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori ORF
Vaccine; probe
                                                                                                                                                                                                     Helicobacter pylori nucleic acids and proteins - used products for the detection, prevention and treatment \epsilon
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                                                                                                                                                                           Claims 27, 31; Page
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                                                                                                                                                                                         nfections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
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11ap20714_4797137_f3_45 cell envelope protein.
12be; diagnostic; ORF; cell envelope protein;
12tein; cellular protein.
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                                                                                                                                                                            207-208; 279pp; English.
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Pred.
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No. 1.
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.58e-112;
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ing them. In all,
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of H. pylori
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                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related prolypeptide(s) - useful for vaccines to treat or prevent H. pylori prolypeptide(s) - useful for vaccines to treat or prevent H. pylori protein.

Prinfection, and to detect Helicobacter

Bisclosure; Page 1363-64; 1481pp; English.

Chiscosure; Page 1363-64; 1481pp; English.

This sequence represents a H. pylori protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified condicted from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                           Matches
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Matches 223; Conservative
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T68226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
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                      156
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                                                                                                                CSPHIIETNEVALKLNYHPASEKVOALDEKILLLRPAFQYSDNIAKEYENKFKNQTTLKV 95
STGLDKMERVLIPAGFVKVTILKPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
                                                                    EEILQNQGYKVINVDSSDKDDESFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 155
                                                 EQILQNQGYKVISYDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGLDKMERVLIPAGFVKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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                                                                                                                                                                                                         h 96.3%;
Similarity 95.3%;
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                     Score 1540; DB 1;
Pred. No. 1.14e-108;
7; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; envelope;
life cycle; activator;
chronic gastritis;
                                                                                                                                                                                       4
                                                                                                                                                                                                                       Length 268;
                                                                                                                                                                              Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an H. pylori derived protein, no further details are given in the specification.

Chearils are given in the specification sequences of the invention of the invention.

Chearils are given in the specification sequences of the invention of the sequence.

Chearils are given in the specification in the pylori nucleic acid sequences, and corresponding proteins, are considered.

Chearils are given in the specification of sequences, and corresponding proteins, are considered.

Chearils are given in the sequences, and corresponding proteins of the sequence.

Chearils are given in the sequences, and corresponding proteins are considered in this protein and interests in the sequences of these sequences are complementary to the stail of the specification of a gene from Helicobacter specification.

Chearils are given in the specification of the sequences of these sequences are complementary to the stail-cut pylori whole genomic DNA was isolated and nebulised to a median size of complementary to the stail-cut pylori while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts of sentences of the sequences of the series of sentences.

Chearily are the series of the series of the series of the sequences are then sequences are the sequences are the sequences are the sequences a
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Best Local S
Matches 4
H. pylori derived protein.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. pylori derived protein.

Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer diseas activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisease; inhibition.
                                                                                                                                                                                 W20454 standard; protein; W20454; Protein; W20454; Protein; Protein; W20454; Protein; W20454; Protein; W20454; Protein; W20454 standard; Protein; W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced.
Note: The ORF/protein reference number for this from the related specification, WO9640893.
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N-PSDB; T77481.
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15-NOV-1996; U18542.
17-NOV-1995; US-561469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
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12-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    53 CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSXNI 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.9%;
larity 97.7%;
Conservative
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27-MAR-1997; U05223.
06-DEC-1996; US-7613
29-MAR-1996; US-6258
02-APR-1996; US-7587
25-OCT-1996; US-7389
28-OCT-1996; US-7388
(ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
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19-DEC-1996:
06-JUN 1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein (The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

DNA and probes derived from it may be used for the identification of
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                                                                                                                                                                                                                                                                                                                                         H. pylori ORF 01ae11010_40688_c2_38 cell envelope OMF.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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08-761318.

08-625811.

08-758731.

08-736905.

08-738859.
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Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection claim 14; Pages 558-559; 1145pp; English.

This sequence is a H. pylori protein of unspecified function. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. DNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nuc
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25-OCT-1996;
28-OCT-1996;
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                                                                                                                                                                                              (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
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Misc_difference 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. pylori ORF hp3e11075orf3 protein. Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacteria; linhibitor; duodenal ulcer disease; chronic ga
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; US-761318.
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are not given in
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No. 3.94e-08;
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gastritis; diagnosis.
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                                                                                                                                                                            Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J; WPI; 98-542293/46.

N-PSDB; X14051

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 8; Page 455-456; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for sequence 240 also per se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. pylori GHPO 1615 proteir GHPO protein; Helicobacter peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(INMER) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
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W98332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNSND-AIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
       14.2%;
larity 25.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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larity 25.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; gastroduodenal disease; gastritis;
Score 227; DB 1; L
Pred. No. 1.46e-07;
75; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 235; DB 1; Length 261;
Pred. No. 3.94e-08;
75; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                        Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
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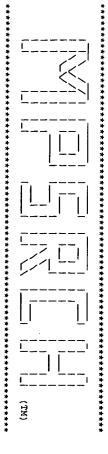
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y10951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 98-271811/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; ce
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acids and proteins - used products for the detection, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9818323-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claims 27, 31; Page 151; 279pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; X30418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori ORF 04ee11108_3906963_f1_7 cell envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 ORFs are shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y10951;
                                                                                                                                                                                                                                                                              121 QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199
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                                                        231 KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                    97
                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                                                                                                                                                                                                                          64 PLDFNY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 120 :| :| | | | | | | | : | ::::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 V-KGTDNSND-AIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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                                                                                                                                                                                                                           KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                   VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-
                                                                                                                                                                   VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                                                                                                                                                                                                                                                                                                            ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVID-M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRTNSGGFVPKTF
-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe; diagnostic; ORF;
protein; cellular protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; U19575.
; US-891928.
; US-739150.
; US-759739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 176; DB 1;
Pred. No. 5.19e-04;
59; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                IQEKFLKTTHSSHSGGLVSTMVKGT-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used
                                                        273
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of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Tue Sep 26 16:20:02 2000; MasPar time 9.81 Seconds 735.665 Million cell updates/sec

Title:

Description: Perfect Score:

Sequence: >US-09-308-435-4 (28-260) from US09308435.pep 1599 1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: PAM 150 Gap 11

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 48.644; Variance 103.561; scale 0.470

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2221188 2222222222222222222222222222222	Result No.
1575 1575 1573 1546 8446 109 109 109 100 100 100 100 100 100 100	Score
0000054 988688666666666666666 474066666666666666666666	Query Match
260 260 260 260 125 616 616 616 616 618 618 618 618 773 1803 311 1803 311 1803 311 773 773	Length
	BG
HPAS_HELPY HPAC_HELPY HPAC_HELPY HPAA_HELAC HPAA_HELAC 173.9_METJA ORC3_YEAST MTNN_MEILA SYEB_MYCON KPC1_NEUCR KPC1_NEUCR RL3_CHLTR RBP2_PLANT RBP2_PLANT RBP2_PLANT LENCU FMT_MYCON FMT_M	ĬĐ
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5.31e-275 7.82e-275 7.82e-275 7.82e-275 7.82e-275 8.64e-133 5.54e-118 2.68e-01 1.04e+00 1.75e+00 2.97e+00 2.97e+00 2.97e+00 3.85e+00 4.97e+00 6.40e+00	Pred. No.

Query Match 99.4%; Best Local Similarity 99.6%; Matches 232; Conservative

Score 1589; DB 1; Pred. No. 5.31e-278; 0; Mismatches 1;

Length 260; Indels

0;

Gaps

0;

4.4 5	42	410	3 3 9 8	36 37	35	ω u 4- u	32	31	30	200	27	26	25	24
94 3	Q Q 4 D	0 Q 12 44	9 9 4 5	9 4 7 7	94	95	95	94	95 6	96	96	96	96	96
51.51 88.90	5.5 9.9		5.9 9.9	5. 5.	5.9	Ф		5.9	Ф С		•		6.0	6.0
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MEDLINE; 97394467.

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Releschmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Relsson K., Ouackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson K., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Berg D.E., Gocayne J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                       EMBL; AE000591; AAD07844.1; -. TIGR; HP0797; -. PROSITE; PS00013; PROKAR_LIPOP
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     Flagella;
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Bacteria; Proteobacteria; epsilon subdivision;
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STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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3; Outer membrane; Lipoprotein; Signal.

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Pred. No. 7
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N-ACTL DIGLYCERIDE (PROBABLE).
N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTEMYIAL).
; 676DDA952E99E03C CRC64;
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Best Local
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    HPAA_HELNE
Q48244;
Q1-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, nucleotide sequence, and expreadhesin subunit protein of Helicobacter J. Bacteriol. 175:674-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93139033.

Evans D.G., Karjalainen T.K., Evans D.J., Gran
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01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR (N-
ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ
BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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larity 95.3%;
Conservative
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                                  STANDARD;
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embrane; Lipoprotein; Signal.
27 BY SIMILARITY.
260 NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ
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8; 1
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N-ACETYL-NEURAMINYL-ALPHA(2,3)-LACTOSE
BINDING MOTIF (POTENTIAL).
; 22489598065E7B14 CRC64;
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1. No. 1.73e-269;
Mismatches 3;
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01-NOV-1997
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PROSITE; P
Flagella;
NON_TER
DOMAIN
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SEQUENCE FROM N.A.
MEDLINE; 96001251.
Evans D.G., Lampert H.C.,
Bronsdon M.A., Evans D.J.
                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-19198 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-
BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
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15-JUL-1998 (Rel. 36, Last annotation update)
NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH)
(FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).
                                                                                                                        Helicobacter acinonyx.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVANS D.G., Lampert H.C., Nakano H., Ea
Bronsdon M.A., Evans D.J. Jr.;
"Genetic evidence for host specificity
"Genetic evidence for host specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 163:97-102(1995).
-!- SUBCELLULAR LOCATION:
ANCHOR (PROBABLE).
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Bacteria; Proteobacteria;
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TE; PS00013; PROKAR_LIPOPROTEIN;
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120; Conser
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Pred.
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                                                                                                                      subdivision;
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No. 8.64e-133;
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Q1-NOV-1997
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                                                                                                                                                                                                     Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";

I yeast 12:693-708(1996).

I regulator protein CFTR.";

C -!- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.

C -!- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS OF 120 KDA, 71 KDA, 62 KDA, 56 KDA, 53 KDA AND 50 KDA.

C -!- SUBCELLULAR LOCATION: NUCLEAR.
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"The multidomain structure o
of DNA replication and trans
Cell 83:563-568(1995).
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or send a
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a continue the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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TIGR; MJ0329; -.
Hypothetical protein.
SEQUENCE 616 AA; 72036 MW
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SEQUENCE FROM N.A.
FY23;
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Hardy C.F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN 62 KDA SUBUNIT).
ORC3 OR OAF1 OR OIF1 OR YLL004W OR L1365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 96405918.
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MEDLINE, 96069857
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on email to license@isb-sib.ch).
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Pred. No. 2.
27; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J., Kobayashi R., Stillman B
Orclp reveals similarity to
riptional silencing.";
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.68e-01
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Best Local
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EMBL; U48888; AAC49270.1; -
EMBL; X91488; CAA62765.1; -
EMBL; Z73109; CAA97447.1; -
SGD; L0003074; ORC3
DNA replication; Nuclear pr
SEQUENCE 616 AA; 72077 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTNX_NEILA
P24581;
01-MAR-1992
01-MAR-1992
15-JUL-1998
                                                                                                                                                                               PRAN; PF00145; DNA_methylase; 1.
PRINTS; PR00105; CSMETTRERASE.
PROSITE; PS00094; CS_MTASE_1; 1.
PROSITE; PS00095; CS_MTASE_2; 1.
Transferase; Methyltransferase; Restriction system.
ACT_SITE 74 74 BY SIMILARITY.
SEQUENCE 313 AA; 34842 MW; E75150C89ABEA611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. NIAIII and a cytosine-type methylase.";

MOL. Gen. Genet. 224:101-110(1990).

-I- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE, CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANDS.

-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

-I- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel.
CYTOSINE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of two tandemly arranged DNA methyltransferase genes of Neisseria lactamica: an adenine-specific
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X54485;
PIR; S12037; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labbe D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria
                                                                                                                                                                                                                                                                                                                                                                  REBASE;
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                           9
EKILLLR-P-AFQYSDNIAKEYENKFKNQTALKVEQI-LQNQGYKVISVDSSDKDDFSFA 112
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                                                                                                                                                                                                                                                                                                                                                                                                            2037; XYNHCL.
                                                                                                Similarity
29; Consen
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                                                                                              6.5%;
llarity 34.9%;
Conservative
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larity 25.7%;
Conservative
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A; 72077 MW; 3F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21, Created)
21, Last sequence update)
36, Last annotation update)
METHYLTRANSFERASE NLAX (EC
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                                                                                      Score 104; DB 1; Le
Pred. No. 1.04e+00;
N4 smatches 27;
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3FAAEE3F645D3F9C CRC64;
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                                                                                                                                          Length
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                                                                                              Indels
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15-FEB-2000 (Rel. 35, Last sequence
PHENYLALANYL-TRNA SYNTHETASE BETA CH
TRNA LIGASE BETA CHAIN) (PHERS).
PHET OR MP049.
                                                                                                                                                                                                                                                                      KPC1_NEUCR STANKELL

KPC1_NEUCR STANKELL

P87253;

P87253;

15-UUL-1999 (Rel. 38, Cr.

15-UUL-1999 (Rel. 38, La.

15-UUL-1999 (Rel. 38, La.

15-UUL-1999 (Rel. 38, La.
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P75563;
                                                              Arpaia G., Macino G
"Molecular cloning
crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000006; AAB95696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                    Submitted
                                                                                                                                                                                                                            Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Nucleic Acids
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STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                            Neurospora crassa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 SLLRVIQK-NAAYKNKLGNIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      506 ALQKLRTKLQTLGFHNVITYQLISPERARNFNLFGLSNLWEIKNP-LSNERSVLRVGLID 564
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         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC.
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SUBUNIT: TETRAMER OF
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PFAM; PF00130; DAG_PE-bind; 2.

PFAM; PF00066; pkinase; 1.

PFAM; PF00433; pkinase_C; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00479; DAG_PE_BINDING_DOMAIN; 2.
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                                                                                                    Stephens R.S., Kalman s
Mitchell W.P., Olinger
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15-FEB-2000 (Rel. 39,
15-FEB-2000 (Rel. 39,
                                                                                                                                         STRAIN-D/UW-3
                                                                                                                                                                                            Chlamydia
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                                                             Science
                                                                        Chlamydia
                                                                                                                             MEDLINE; 99000809.
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                                                                                                                                                                                                                                                                                                                         102 DSSDKDDFS-FAQKKEGYLAVAMNGEIVLRPDPKR 135
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              SIMILARITY: BELONGS
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                                                                                                                                                                                                                  RIBOSOMAL
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SIMILARITY:
                       THE RIBOSOME (BY SIMILARITY)
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                                                                                               R.W.;
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                                                          la trachomatis.";
282:754-759(1998).
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POLY-GLN.
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L., Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poehlmann R., Philippsen P.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ATP + L-CYSTEINE + TRNA(CYS) = AMP
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01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
putative CYSTEINYL-TRNA SYNTHETASE C29E6.06C
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                                                                                                                                                                                                             EMBL; 271523; CAA96154.1; -. 
PFAM; PF01406; tRNA-synt_1e; 1. 
PRINTS; PR00983; TRNASYNTHCYS.
                                                                                                                                                                                                                                                                      EMBL; X96722; CAA65497.1; -. EMBL; Z71523; CAA96154.1; -.
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
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                                                                                                                                                                                          PROSITE;
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                                                                                                                                                      ypothetical
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                        FSU.

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Similarity 36.7%;
18; Conservative
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97377992.
                                                                                                                                                                                 PS00178; AA_TRNA_LIGASE_I; FALSE_NEG
                                                                                                                                                   protein; Aminoacyl-tRNA
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13; 1
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Pred. No. 2.97e+00
"HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
; 495D526781B4BE2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    065BBC1462353F5B CRC64;
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                                                                                                                                                   synthetase;
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                                                                                                                                                Protein biosynthesis;
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Query Match

SIMILAR BINDING

SEQUENCE

767

AA;

87530 MW; 6.3%;

Score 101;

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Length 767;

Best Local Similarity 27.7%; Matches 18; Conservative

Pred. No. 2.29e+00; 16; Mismatches 26;

Indels

5

Gaps

4

EKVQALDEKILL-LRPAFQYSDNIAKEYENKFKNQTALKVEQIL-Q--NQGYKVISVDSS 104

5 B 5 B

105 DKDDF 109

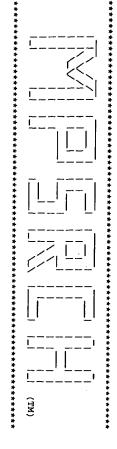
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49

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RESULT
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Best Local
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YJL3_YEAST STANDARW,
P47024; P87192;
01-FEB-1996 (Rel. 33, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
1748 OR YJL113W OR JO780.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBP2_PLAVB STAN
Q00799;
01-APR-1993 (Rel. 2
01-APR-1993 (Rel. 2
01-OCT-1996 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELJ
SEQUENCE FROM N.A.
MEDLINE; 92315338.
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
Galinski M.R., Medina protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN RETICULOCYTE CELLS.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium vivax (strain Belem).
Eukaryota; Alveolata; Apicomplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            759 FESKNNVVLETENMSKNINELDVHKNIQD-AYKV-ALEILAHSDEIDTKQKDSSKL-IEM 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816 GNQIYLK 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 6.3%;
Local Similarity 29.9%;
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQYSDNIAKEYENKFKNQTALKVEQILQNQGYKVISVDS-SDKDDFSFAQKKEGYLAVAM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGEIVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (San email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 125
1251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 1;
Pred. No. 2.97e+00;
17; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no rest
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MBL outstation -
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                                                                                                                    В
                                                                                                                                                       Query Match 6.3%;
Best Local Similarity 24.4%;
Matches 20; Conservative
                                        1231
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                                                                                                            1171 NIKELKVIDKNVPIDNGINVSPRLEQNIEASGSPVQIVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                    Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8D52D3
                                                                                                                                                                                                                                                                             EMBL; Z49389; CAA89409.1; -
                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / FY1679;
MEDLINE; 97103775.
                                                                             183
    240
                                      DKNNSLTSYELERDKKRSKKNR 1252
TOKN-LESYOKDAKELKGKRNR
                                                                             DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KRA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                       Pred.
28; N
                                                                                                                                                                             Score 100; DB 1;
Pred. No. 2.97e+00;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions
                                                                                                                                                       30;
                                                                                                                                                                                             Length 1803;
                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRK1, PBS2,
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                                                                                                                                                       Gaps
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Search completed: Tue Sep 26 16:20:13 2000 Job time : 11 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Tabular output not generated. Tue Sep 26 16:15:28 2000; MasPar time 15.30 Seconds 718.193 Million cell updates/sec

Description: Perfect Score: Sequence:

Title:

Scoring table: >US-09-308-435-2 (28-260) from US09308435.pep 1594 1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

PAM 150 Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 47.512; Variance 117.669; scale 0.404

#### SUMMARIES

22221187 2322223333333333333333333333333333333	Result
1580 843 766 232 1171 1101 1108 1108 1109 1109 1109 1109 110	Score
0.000 0.000	Query Match
260 260 249 249 249 249 249 249 249 249 249 249	Length 1
$\alpha$	B
C71896 PC4099 PC409	ij
adhesin A - Helicobac neuraminyllactose-bin adhesin A - Helicobac adhesin A - Helicobac probable neuraminylla probable neuraminylla probable neuraminylla hypothetical protein TyB protein - yeast (hypothetical protein (Pagellar p	Description
1.16e-237 6.15e-235 2.25e-1100 4.54e-16 6.09e-15 5.00e-08 9.69e-07 1.00e+00 2.63e+00 2.63e+00 3.33e+00 3.33e+00 4.22e+00 4.22e+00 4.22e+00 4.22e+00 6.74e+00 6.74e+00 1.07e+01 6.74e+00 1.07e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ü	32	31	30	29	28	27	26	N U	24
96	96	96	96	97	86	98	98	98	86	97	98	99	99	99	100	101	100	101	101	101	101
6.0	6. O	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	σ. ω	6.3	6.3	6. <sub>3</sub>	6. <sub>3</sub>	6.3	6.3
1265	672	368	231	9376	980	764	705	330	311	308	119	1467	1134	405	1252	1000	856	767	592	571	471
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	ຎ	N	N	Ŋ	N	N	N
F71429	F65096	A28825	D64486	T14593	S54986	B64570	S54521	S58255	S73625	C75125	PL0089	PC1253	D75014	T10260	B42771	T13636	C71956	S63220	G69159	F70040	S54460
₽-	NADH-	keratin, type I nonep	hypothetical protein	syringomycin syntheta	regulatory protein -	phenylalaninetRNA l	probable membrane pro	hypothetical protein	methionyl-tRNA formyl	gmp synthase, cter do			hypothetical protein	patatin-like protein	reticulocyte-binding	probable minor struct	probable endopeptidas	probable membrane pro	sensory transduction	sulfite reductase hom	hypothetical protein
2.64e+01	2.64e+01	2.64e+01	2.64e+01	2.11e+01	1.69e÷01	1.69e+01	1.69e+01	1.69e+01	1.69e+01	2.11e+01	1.69e+01	1.34e+01	1.34e+01	1.34e+01	1.07e+01	8.50e+00	1.07e+01	8.50e+00	8.50e+00	8.50e+00	8.50e+00

# ALIGNMENTS

#accession B47052 ##status pr ##molecule_type DN ##residues 1- ##cross-references	#authors #journal #title #cross-referen	##status ##residues ##cross-ref ##experimen	#journal #title #cross-referen #accession		DATE ACCESSIONS REFERENCE #authors	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM
B47052  preliminary  preliminary  1-2,'T',4,'G',6-18,'T',20-61,'K',63-83,'T',85-88,'E',  90-99,'N',101-108,'F',110-111,'A',113-152,'L',154-179,  'LEWI' ##label EVA1  ferences GB:X61574; NID:9732735	#4/032 #authors Evans, D.G.; Karjalainen, T.K.; Evans Jr., D.J.; Graham,  D.Y.; Lee, C.H. #journal J. Bacteriol. (1993) 175:674-683 #title Cloning, nucleotide sequence, and expression of a gene #title encoding an adhesin subunit protein of Helicobacter pylori. #cross-references MOID:93139035	##status nucleic acid sequence not shown; translation not shown ##molecule_type DNA 1-260 ##label TOM 1-260 ##label TOM ##cross-references GB:AE00051; GB:AE000511; NID:g2313918; PID:g2313925; TIGR:HP0797 TIGR:HP0797	#journal Nature (1997) 388:339-547 #title The complete genome sequence of the gastric pathogen #cross-references MIID:97394467 #accession E64619	Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; MCKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weddman, J.M.; Fujlii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.	09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Feb-1999 E64619; B47052; C47052; PC4088 A64520 Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;	

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ACCESSIONS
REFERENCE
#authors
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FEATURE
134-139
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                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Best Local
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#cross-references
#accession C718
##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:96001251 #accession PC4088
                                                                                                  #journal
                                                                                                                                                                                                                                                                                                        #variety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status preliminary
##molecule_type DNA
##residues 'MR',204-218,'R',220,'LC',223-228,'RS',231-234,'M',
##cross-references GB:X61574; NID:973275-260 ##label EVA2
##cross-references GB:X61574; NID:973275-260 ##label EVA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230;
             A71800
Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D. Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature (1999) 397:176-180
Genomic sequence comparison of two unrelated isolates of thuman gastric pathogen Helicobacter pylori.

ferences MUID:99120557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%;
Similarity 98.7%;
                                                                                                                                                                                                                                                                                               #type complete
neuraminyllactose-binding hemagglutinin
Helicobacter pylori (strain J99)
#formal_name Helicobacter pylori
strain J99
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                                                                                                                                                                                                                                                               12-Feb-1999 #sequence_revision 12-Feb-1999 12-Feb-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43-61,'K',63-83,'T',85-88,'E',90-99,'N',101-108,'F',
110-111,'A',113-123,'I',125-166 ##label EVA3
   preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #region receptor binding #status predicted the 260 #molecular-weight 29040 #checksum
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NCBIP:123534); sequence inconsistent with the nucleotide translation
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Pred. No. 1.16e-237;
3; Mismatches 0;
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                                                                                                                                Query Match 52.9%;
Best Local Similarity 96.0%;
Matches 119; Conservative
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Best Local Similarity
Matches 225; Conser
                                                                                                                                                                                                                                                                                                                      #journal #title
                                                                                                                                                                                                                                                                                #title Genetic evidence for host specificity in the adhesin-encoding genes has of Helicobacter acinonyx, hnaA of H. nemestrinae de di hpaA of H. pylor1.
                                                                                                                                                                                                                                                                         #accession
 163
                                            103
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##residues 1-124 ##label
##cross-references GB:U27127
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                                                                                                         NYHPASEKYQALDEKILLLRPAFQYRDNIAKEYENKFKNQTTLKVEQILQNQGYKVINVD 60
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166
                                                                                                                                                                                                                                                                                                                   A.P.; Bronsdon, M.A.; Evans Jr., D.J.
Gene (1995) 163:97-102
Genetic evidence:
                                                                                                                                                                                                                                                                                                                                                                                                                      ruquby #type fragment
adhesin A - Helicobacter nemestrinae (fragment)
HnaA protein
                                                                                                                                                                             #region receptor binding #status
#length 124 #checksum 6484
                                                                                                                                                                                                                 hnaA
                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Helicobacter nemestrinae
14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
18-Sep-1998
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larity 96.6%;
Conservative
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#length 260 #molecular-weight 29199
                                                                                                                                 Score 843; DB 2; L
Pred. No. 2.25e-113;
4; Mismatches 1;
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Pred. No. 6.15e-235;
7; Mismatches 1;
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##molecule_type DNA
                                                      #gene
                                                                                                                                                                        #title Genomic sequence comparison of two unrelated isolates of human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
#accession E71865
                                                                                                                                                                                                                                             #journal
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                                                                                                      ##residues 1-249 ##label ARN
##cross-references GB:AE001526; GI
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##cross-references GB:U27126
                                                                                      ##experimental_source strain
                                                                                                                                      ##molecule_type DNA
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Similarity 85.5%;
106; Conservative
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Nature (1999) 397:176-180
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Helicobacter pylori (strain J99)
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Gene (1995) 163:97-102
                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Helicobacter
strain J99
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                                   #length 249
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14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
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                                                                                                                                                          preliminary
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rth 124  #checksum 6624
   14.48;
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Helicobacter acinonyx (fragment)
                                 #molecular-weight 28513
   Score
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Pred. No. 1.26e-100;
14; Mismatches 4:
                                                                                      J99
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Matches 57; Conservative
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    210
                                              199
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TIGR:HP0410
X #length 249 #molecular-weight 28349 #checksum 9957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residues 1-249 ##label_TOM
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V-KGTDNSND-AIKSALNKIFANIMGEIDKKLTOKNLESYQKDAKELKGKRN
                      VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                   DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                     QNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGL 151
                                                                                                                                                                                                         ERKGYSV-S-QFKDASEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E- 142
                                                                                                                                                                                                                                                       ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL 91
                                                                                                                                                                                                                                                                                                 NTGESVELHFHY-PIKGKQEPKNSHLVVLIEPKIEINKVIPESYQKEFEKSLFLQLSSFL 93
                                                                                                          EKVID-M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRINSGGFVFKTF 198
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                                                                                                                                                                                                                                                                                                                                           h 13.9%;
Similarity 25.0%;
58; Conservative
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Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen Helicobacter pylori.
erences MUID:97394467
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Helicobacter pylori (strain 26695)
#formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 15-Aug-1997 #text_
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Local Similarity 25.1%;
hes 56; Conservative
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#cross-references GB:AE001479; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
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              Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Veneer, J.C.
Nature (1997) 388:539-547
                                                                                                                                                                                                                                                                                                                                        #formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 0
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26695)
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#length 282 #molecular-weight 32075 #checksum
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Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge,
B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
G.F.; Trust, T.J.
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11 protein HP0492 – Helicobacter
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Pred. No. 5.00e-08;
58; Mismatches 91
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                                                                                                                                                                                    1170 NLKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKBKRH 1229
                                                                                                                                     1230 DKNNSLTSYELERDKKRSKRNR 1251
                                                                                                         240
                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-1802 ##label
##cross-references EMBL:U11581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 QVLRFQD-EKA-LNAQDKRKIFSVLDLKGWVGILEDLKMNL--K-DPN---NPNLDTL-- 168
                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 D-NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 EKNKEDAIHKILNRMYAVVMKKAVTELTKENIDKYREAIDRMKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 VLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGL-VS-TMVKG-T 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:AE000564; GB:AE000511; NID:g2313602; PID:g2313613;
                                                                                                                                                                                                                                                    Match 6.9%;
Local Similarity 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 25.0%;
tes 56; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PLDENY-PI-HIVQAPQNHHVVGILTPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 118
                                                        10
                                                                                                                                                                  DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                      TQKN-LESYQKDAKELKGKRNR 260
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hypothetical protein PAB0993 - Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                         S5261
                                                                                                                                                                                                                                                                                                                                                                                                                                     Favello, T.
submitted to the EMBL Data Library, the sequence of S. cerevisiae cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retrotransposon Ty4
protein YHLO08w-a
#formal_name Saccharomyces cerevisiae
05-May_1995 #sequence_revision 19-Oct-1995 #text_change
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Pred. No. 1.00e+00;
27; Mismatches 29
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Pred. No. 9.69e-07;
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                      Pyrococcus
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                                                                                                                                                                                                                                                                     Length 1802;
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                  abyssi
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                    (strain
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ORGANISM

#formal\_name

Pyrococcus abyssi

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##cross-references SGD:S0003927; MIPS:YLL004w #map_position 12L SUMMARY #length 616 #molecular-weight 72076
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 Query Match
Best Local Similarity
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Best Local Similarity 24.7%;
Matches 21; Conservative
                                                                                                     #gene
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#journal
#title
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                                                                                                                           ##residues 1:616 ##label MIW
##cross-references EMBL:X91488; NID:g1495203; PID:e199016; PID:g1495220
##note the nucleotide sequence was submitted to the EMBL Data
Library, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:273109; NID:g1360162; PID:e245444; PID:g1360163; MIPS:YLL004w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 ERMFSFPLEIAE-SLEKRLIKSLEK-RVEELVEEKVKNSNNGISPEVIREFIDK-YDSLV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:AJ248287; GB:AL096836; NID:g5458657; PID:G5458916
                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                      ##status
                                                                                                                                                                                                                                                                                                                                                                                                    ##experimental_source strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 QEIDKKLTQKNLESYQKDAKELKGK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 RE-NVEL-RRRLESREKIIKDLREK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 ESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNS-N-DAIKSALNKIFANIM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
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ORC3 protein - yeast (Saccharomyces cerevisiae)
protein L1365; protein YLL004w
#formal_name Saccharomyces cerevisiae
01-Aug-1995 #sequence_revision 24-May-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anonymous, Genoscope
submitted to the EMBL Data Library, July 199
submoteries abyssi genome sequence: insights
Pyrococcus abyssi genome sequence:
                                                                                                                                                                                                                                     S70572
                                                                                                                                                                                                                                                                              Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Protein Sequence Database, May 1996 S64746
                                                                                                      SGD:ORC3; OAF1
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                                                                                                                                                                                                                                                                                                                                                    Miosga, T.; Zimmermann, F.K.
Yeast (1996) 12:693-708
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#length 320 #molecular-weight 37677
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                                                                                                                                                                                                                nucleic acid sequence not shown; translation
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   6.7%;
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Pred. No. 1.63e+00;
32; Mismatches 25;
   Score 107;
Pred. No.
   2.07e+00;
                  Length 616
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ACCESSIONS
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 DPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-394 ##label KLE
##cross-references GB:AE001137; GB:AE000783; NID:g2688160; PID:g2688181;
TIGR:BB0285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##experimental_source strain B31
Y #length 394 #molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 EYENKFKNQTALKVEQILQNQGYKVISVDSSDKDDFSFAQK-KE-GYLAVANNGEIVLRP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                366
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Similarity 19.7%;
24; Conservative
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                                                                                                                                                                                     $73374  #type complete
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain pheT -
Mycoplasma pneumoniae (AFCC 29342) (SGC3)
hypothetical protein C09_orf805; phenylalanyl-tRNA synthetase
  Himmelreich, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C. Rature (1997) 390:580-586
                                                                                         26-Feb-1997_#sequence_revision
                                                                                                                                                  #formal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E70135 #type complete flagellar protein (flbC) homolog - Lyme disease spirochete #formal_name Borrella burgdorferi #common_name Lyme disease
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                                                                          16-Jul-1999
                                                                                                                                                                      beta chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence
                                                                                                                                             _name Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #sequence_revision 13-Feb-1998 #text_change
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Pred. No. 2.63e+00;
44; Mismatches 48
Hilbert,
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H.;
Plagens,
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Pirkl,
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RESULT
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SUMMARY
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##molecule_type DNA
##residues 1-1465 ##label JAN
##cross-references EMBL:S46865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #cross-references MUID:93015829
#accession S31262
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#title
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                                                                                                                                                                                                                                                                                                                                                         #mobile_element retrotransposon Ty4

MARY #length 1465 #checksum 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
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#accession $73374
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                                                                                                                                                                                                                       565 SLLRVIQK-NAAYKNKLGNIF 584
                                                                                                                                                          893 DKNNSLTSYELERDKKRSKKNR 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 ALQKLRTKLQTLGFHNVITYQLISPERARNFNLFGLSNLWEIKNP-LSNERSVLRVGLID 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:AE000006; GB:U00089; NID:g1673695;
PIDN:AAB95696.1; PID:g1673698
the nucleotide sequence was submitted to the EMBL Data
Library, November 1996
                                                                                                                        240 TOKN-LESYQKDAKELKGKRNR 260
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                                                                                                                                                                                                DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
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Similarity 28.4%;
23; Conservation
                                                                                                                                                                                                                                                                             h 6.6%;
Similarity 25.6%;
21; Conservative
S56894 #type complete
TyB protein - yeast (Saccharomyces cerevisiae)
retrotransposon Ty4.JL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyB protein - yeast (Saccharomyces cerevisiae)
retrotransposon Ty4 (fragment)
#formal_name Saccharomyces cerevisiae
18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily phenylalanine--tRNA ligase beta chain aminoacyl-tRNA synthetase; ligase; protein biosynthesis #length 805 #molecular-weight 91713 #checksum 4320
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Nucleic Acids Res. (1996) 24:4420-4449

Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ty4, a new retrotransposon flanked by tau-elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Janetzky, B.; Lehle, L.
J. Biol. Chem. (1992) 267:19798-19805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S31262 #type fragment
TyB protein - yeast (Sacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-Apr-1997
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                                                                                                                                                                                                                                                                             Score 105; DB 2; Length 146
Pred. No. 3.33e+00;
28; Mismatches 29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae
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                                                                                                                                                                                                                                     Query Match 6.6%;
Best Local Similarity 25.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                              #mobile_element retrotransposon Ty4.JL
MARY #length 1803 #molecular-weight 207708 #checksum
                                                                                                                                                                                                                                                                                                                                                         #map_position 10L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
                                                                                                                                                                                  1171 NIKELKVTDKNVPTDNGTNVSPRLEQNIEASGSPVQTVNKSAFLNKEFSSLNMKRKRKRH 1230
                                                                                                                   1231 DKNNSLTSYELERDKKRSKKNR 1252
                                                                                                                                                        183 DLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAI-KSA-LNKIFANI-MQEIDKKL 239
                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##residues 1-18
                                                                               240 TQKN-LESYQKDAKELKGKRNR 260
                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-1803 ##label CZI
MIPS:YJL113w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein J0780; protein YJL113w
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cziepluch, C.; Kordes, E.; Pujol, A.; Jauniaux, J.C. submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S56891
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Pred. No. 3.33e+00;
28; Mismatches 29;
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(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Tue Sep 26 16:14:59 2000; MasPar time 9.09 Seconds 606.971 Million cell updates/sec

Description: Perfect Score: Title: >US-09-308-435-2
(28-260) from US09308435.pep
1594
1 CSPHIIETNEVALKLNYHPA.....QKNLESYQKDAKELKGKRNR 233

Scoring table: Sequence: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

Searched:

188963 seqs, 23686106 residues

Database:

a-geneseq36 1:geneseqp

Statistics: Mean 32.420; Variance 175.543; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1594 1589 1589 1582 1545 302 302 302 302 230 230 231 171 171 171 177 107 107 107 100 100 10	1594	Score
1100 9997 9974 11444 1007 1007 1007 1007 1007 1007 1		Query Match 1
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Adhesin/V.cholerae tox Helicobacter pylori su Helicobacter pylori derived prot Helicobacter pylori derived prot Helicobacter clight Herozoite apical-end-helicobacter clight Herozoite apical-end-lo Pasteurella multocida	Helicobacter pylori 29	Description
4.75e-113 1.18e-112 9.72e-1110 3.46e-109 5.42e-13 5.42e-13 5.42e-13 8.55e-08 8.55e-08 8.55e-08 3.16e-07 1.10e-03 1.10e-03 1.10e-03 1.10e+01 1.60e+0	=:	Pred. No.

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5. 9	5.9	5.9	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1			6.1			
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R71011	W63145	R33553	R71015	W02616	R39266	W49814	W56319	W56322	R72386	W95018	W60213	W33807	W24800	W98549	W49816	R43339	W49818	R39268	W49817	R39267	W49813
_	Human calcium channel	Sequence of the alpha	Human neuronal calcium	Wheat adenylosuccinate	Mouse C4G1 Ig heavy-ch	ຜ		hīlus paragal	fth	x tran	Spinocerebellar ataxia	Human ataxin-2.	Spinocerebellar ataxia			Completely humanised C		Humanised C4G1 Ig heav	=	Humanised C4G1 Ig heav	Amino acid sequence of
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## ALIGNMENTS

Ş 밁 Query Match 100.0%; Best Local Similarity 100.0%; Matches 233; Conservative Score 1594; DB 1; Length 260; Pred. No. 4.75e-113; 0; Mismatches 0; Indels Indels 0; Gaps

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88 EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori surface exposed antigen - useful for treatment, prophylaxis or diagnosis of mammalian infections (laim 2; Page 34-35; 49pp; English.

Ke Laim 2; Page 34-35; 49pp; English.

Ke A 29 kDa antigen (W07449) of Helicobacter pylori is an adhesin expressed on the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43835) differs only at position 222 (Arg for Ser). Recombinant antigen can be produced in transformed host cells. It is useful for the diagnosis and treatment of H. pylori infections and for use as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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05-DEC-1996; SE0727.
03-JUN 1996; SE-002007.
01-JUN-1995; SE-001085.
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therapy;
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Bolin I, Svennerholm
WPI; 97-034307/03.
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STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
                                                                                                                 STGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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                                                                                                                                                                                                                                                                                                                 CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV
                                                                                                                                                                                          EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
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Similarity 100.0%;
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28. .260
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25. .28
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peptidase II in prolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ori strain CCUG 17874 (NTCC 11637).
Location/Qualifiers
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Pred.
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No. 4.75e-113;
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PT useful in the diagnosis and treatment of H. pylori
PS Claim 2; Page 20-21; 32pp; English.

CC This sequence represents the fusion protein of the invention, between the
CC This protein is used in the diagnosis of and as a vaccine against
CC This protein is used in the diagnosis of and as a vaccine against
CC Unicers. It may also be used in the production of an anti-H. pylori
CC antibody. Vectors containing the DNA sequence and E. coli strains
CC containing it form the basis of a process to produce the protein; which
CC consists of culturing the microorganism and obtaining the protein: The
CC protein is an effective vaccine against H. pylori due to its excellent
CC immunogenicity for H. pylori, stability within the stomach environment,
CC and its ability to penetrate through the stomach mucous membrane to
CC stimulate sigh production.
                   W60157 standard; Protein; 260 AA.
W60157;
28-SEP-1998 (first entry)
Helicobacter pylori 29 kDa surface-exposed an
Cell surface antigen; adhesin; infection; vac
Helicobacter pylori.
W09822135-A1.
28-MAY-1998.
18-NOV-1997; SE1927.
22-NOV-1996; SE-004296.
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Best Local 9
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21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO
Kim BO, Lee BK, Park SK, Y
WPI; 98-434925/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: This sequence was indexed from WO9853082, which is the first major country equivalent to KR97059278.
Sequence 461 AA;
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Adhesin/V.cholerae toxin A2 and B subunit fusion grashion gene; V.
Fusion gene; H. pylori infection; adhesin gene; V.
A2 subunit; B subunit; diagnosis; vaccine; gastrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Vibrio W09853082-A1.
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Chimeric - Heli
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18-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene consisting of the Helicobacter pylori adhesin gene to the A2 and B subunit gene of Vibrio cholerae toxin in the diagnosis and treatment of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%;
L Similarity 100.0%;
233; Conservative
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Pred. No. 4.75e-11;
0; Mismatches (
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                                                                                                                                                        vaccine;
                                                                                                                                                                                    antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
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1997; SE1927. 1996; SE-004296. ASTRA AB.

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This polypeptide comprises a 29 kDa surface antigen which is carperssed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is and is also a putative virulence factor. The invention relates to an ey pharmaceutical composition comprising a lipid aggregate of a new pharmaceutical composition comprising a lipid aggregate of a negatively charged lipid or lipid mixture and at least one antigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see V3464) coding for such an antigen. The new formulations, which are useful as vaccine formulations, elicit a protective immune response capainst H. pylori infections, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second, claimed 29 kDa antigen (see W60156) is provided that differs only at residue 222 (ser for Arg).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 23
            WO9638475-A1.
05-DEC 1996; SE0727.
03-JUN-1996; SE-002007.
21-MAR-1996; SE-001085.
(ASTR ) ASTRA AB.
Bolin I, Svennerholm A;
                                                                                                                                                                                                                                                                              Antigen; adhesin; in therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aggregate of negatively charged lipid and Helicobacter pylori antigen - useful in therapeutic or preventative vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berglindh T, Lofroth WPI; 98-312174/27. N-PSDB; V34643.
                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                             cleavage_site
                                                                                                                                                                                                                                                                         Helicobacter
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                                                                                                                                                                                                                                                                                                                                                               W07450 standard;
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 1 I, Svennerholm A;
97-034307/03.
                                                                                                                                                                                                                                                                                                                                                                                                                      TMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                forms of bacterium, to generate systemic and mucosal antibody
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Similarity 99.6%;
232; Conservative
                                                                                                                                                                                                                                                      pylori strain CCUG 178:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                              /note= "consensus recognition site for signal peptidase II in prolipoproteins" 28. .260
                                                                                                                      /note-
                                                                                                                                              /label=
                                                                                                                                                                                                                         'label = Sig_peptide
                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                     immunogen;
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*either the '
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Pred. No. 1.18e-112;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                  kDa antigen.
immunisation; ulcer;
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Best Local S
Matches 23
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CA 29 kDa antigen (W07450) of Helicobacter pylori is an adhesin conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. Of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07549) deduced from a second cDNA clone (T43834) differs only at position 222 (Ser for Arg). Recombinant cantigen can be produced in transformed host cells. It is useful for the diagnosts and treatment of H. pylori infections and for use as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1998.
28-OCT-1997; U19575.
14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
                    Claims 27, 31; Page 207-208; 279pp; English.

Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999 (first entry)
H. pylori ORF llap20714_4797137_f3_45 cell envelope protein.
Vaccine; probe; diagnostic; ORF; cell envelope protein;
secreted protein; cellular protein.
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Alm RA, Smith D;
WPI; 98-271811/24.
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  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Hellcobacter pylori nucleic acids and proteins - used products for the detection, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-271811/24.
N-PSDB; X30467.
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                                                                                                                                                                                                                                                                                                                                                                                                                        ps Disclosure; Page 1333-64; 1481pp; English.

This sequence represents a H. pylori protein.

This sequence represents a H. pylori protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds; useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori aby PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. infection, and to detect Helicobacter
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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Pred. No. 3.46e-109;
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life cycle; activator;
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CC Helicobacter pylori has been strongly linked to chronic gastritis and CC duodenal ulcer disease. The nucleic acid sequences of the invention CC are used to evaluate compounds, especially activators or inhibitors of CC bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are CC expense. The nucleic acid sequences, and corresponding proteins are CC used to inhibit expression of a gene from Helicobacter species in CC a sample. Antisense nucleic acid sequences of these sequences are Used to inhibit expression of a gene from Helicobacter species. H. CC pylori whole genomic DNA was isolated and nebulsed to a median size of BSTXI-linker adapters in 100-1000 fold molar excess. These linkers are CC complementary to the BSTXI-cut pMPX vectors, while the overhang is not complementary. Therefore the linkers will not concatemerise nor CC will the cut vector re-ligate itself easily. The linker-adapter inserts shotoun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query match
Best Local S
Matches 4
H. pylori derived protein.

Gytoplasmic; vaccine; prevention; treatment; infection; identification; Cytoplasmic; vaccine; prevention; life cycle; activator; bacteria; inhibitor binding compound; bacterium; life cycle; activator; bacteria; inhibitor duodenal ulcer disease; chronic gastritis; diagnosis; envelope. Helicobacter pylori.
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W24663;
W24663;
12-AUG-1997
                                                                                                                                                                                                                   W20454 standard;
W20454;
                                                                                                                                                                                    29-JUL-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequenced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith DH;
WPI; 97-298052/27.
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17-NOV-1995; US-561469.
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                                                                                                                                                                                                                                                                                                                                                            CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNI
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larity 97.7%;
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Pred. No. 5.42e-13;
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                                                                                       bacteria; inhibitor;
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Best Local S
Matches 4
                                                                                                                                                                                                                      09-OCT-1997.

27-MAR-1997; U05223.

06-DEC-1996; US-761318.

29-MAR-1996; US-625811.

02-APR-1996; US-758731.

25-OCT-1996; US-736905.

28-OCT-1996; US-738859.
                                                                                                                                                           (ASTR) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
N-PSDB; V24854.
      Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein (The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. DNA and probes derived from it may be used for the identification o
                                                                                                                                                                                                                                                                                                                                   unnibitor; duodenal ulcer
Helicobacter pylori.
W09737044-Al.
                                                                                                                                                                                                                                                                                                                                                                    4-UN-1996 (LILES COLD)
H. pylori ORF Olael1010_40688_c2_38 cell envelope OMP.
Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastrifis; di
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W55445
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The present sequence is a H. py
are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and polypeptide(s) - useful for vaccines to treat
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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infection, and to detect Helicobacter
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19-DEC-1996.
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43; Conse
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larity 97.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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Pred.
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1. No. 5.42e-13;
1. No. 5.42e-13;
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Best Local
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09-OCT 1997; U05223.
27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-73873.
25-OCT-1996; US-738859.
N-PSDB; V24741.

N-PSDB; V24741.

Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claim 14; Pages 558-559; 1145pp; English.

This sequence is a H. pylori protein of unspecified function. This sequence is a H. pylori protein to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacteria; linhibitor; duodenal ulcer disease; chronic ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori in acid sequence
                                                                                                                                                                                                                                                                                                                                                       Alm RA,
                                                                                                                                                                                                                                                                                                                                                          (ASTR ) ASTRA
Alm RA, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W55332 standard;
W55332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori ORF hp3el1075orf3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY
                                                                                                                                                                                                                                                                                                                             97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRINSGGFVPKIFVHRIK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SV-S-QFKDVSEIFQDIKEKALLVLRWDGNVAI-LE-D-IVEE-SDA--L-S-E-EKVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT
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57; Conser
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llarity 25.18;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                          D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sample and the diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "the nucleotides encoding are not given in the spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 230; DB 1;
Pred. No. 8.55e-08;
74; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t; infection; envelope;
; life cycle; activator
gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ding this amino specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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Best Local S
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01-APR-1998, U06371.

29-JUL-1997, US-902615.

01-APR-1997, US-833457.

24-JUN-1997, US-881227.
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                                                                                                                                                                                New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 8; Page 455-456; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also used for the production of antibodies. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori GHPO 1615 protein.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HDMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptic ulcer disease
Helicobacter pylori.
WO9843478-Al.
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w98332;
31-MAR-1999 (first entry)
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; X14051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -M-SSGYLNINFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRTNSGGFVPKTFVHRIK 215
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Similarity 25.1%;
57; Conservative
                                                                                                                                                               249 AA;
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                       13.9%;
llarity 25.0%;
Conservative
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Pred. No. 8.55e-08;
74; Mismatches 74
                       Score 222; DB 1; Le
Pred. No. 3.15e-07;
74; Mismatches 77;
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                                                                                     Length 249;
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                    Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleic acids from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; cellular protein.
Helicobacter pylori.
W09818323-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. pylori ORF 04ee11108_3906963_f1_7
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Y10951;
Y10951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claims 27, 31; Page 151; 279pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acids and products for the detection, prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alm RA, Smith D;
WPI; 98-271811/24.
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Alm RA, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1997; U19575
14-JUL-1997; US-891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; probe; diagnostic; ORF; cell envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1999
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                                                                                                                                                                                                                                                                                         121
                                                    231 KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
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                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                     39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY
                                                                                                                                                                                                                                                                                                                                                                     64 PLDENY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY : | : | | | | | | | : | : | ::::||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                              VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                                                                                                                                                                                         KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
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-NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                            VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
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56; Conser
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US-739150.
US-759739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection, prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 171; DB 1; L
Pred. No. 1.10e-03;
58; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $
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H. pylori
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PS Claim 72; Page 1333-1334; 1481pp; English.

CC The present sequence is a H. pylori secreted or periplasmic protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors.

CC useful as potential H. pylori life cycle activators or inhibitors.

CC the genomic sequence of H. pylori (ATCC 55679) was determined from

CC overlapping contigs generated by mechanically shearing the bacterial

CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,

CC identify likely H. pylori antigens for vaccine development, the amino

CC acid sequences predicted from various ORF were analysed for significant

CC homology to other known or exported membrane proteins. Having identified

CC and determined the sequences of interest, particular regions can be

CC isolated from H. pylori by PCR amplification for recombinant polypeptide

CC production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 5
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H. pylori secreted or periplasmic protein, 27zel035lorf5.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; diuddenal ulcer disease; chronic gastritis; diagnosis; envelope.
19-DEC-1996.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
                                                                                               Helicobacter pylori. W09640893-A1.
                                                                                                                                                                                              H. pylori secreted or peripplsmic protein, 3906963.aa. Cytoplasmic; vaccine; prevention; tracatment; infection; envelope; identification; binding compound; bacterium; life cycle; activato bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent
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(ASTR ) ASTRA AB.
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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W20938 standard; protein;
                                                                                                                                                               diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                     T 15
W20468 standard; Protein; 147
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WO9640893-Al.
                                                                                                                                                                                                                                                                                                                                                                    W20468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKMNL--K-DPN---SPNLDTL-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 10.7%;
Local Similarity 25.1%;
les 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
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problypeptide(s) - useful for vaccines to treat or prevent H. pylori prinfection, and to detect Helicobacter

Problypeptide(s) - useful for vaccines to treat or prevent H. pylori prinfection, and to detect Helicobacter

Problypeptide(s) - useful for vaccine to prevent or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori CC Infection or to identify H. pylori polypeptide binding compounds, consecution or to identify H. pylori (ATCC 55679) was determined from CC useful as potential H. pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino CC acid sequences predicted from various ORF were analysed for significant CC homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be collated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berglindh
WPI; 97-05
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(ASTR ) ASTRA AB
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N-PSDB; T67633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and
polypeptide(s) - useful for vaccines to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D,
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Length 147;
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Š 밁 ₽ Query Match Best Local Matches 121 97 39 64 PLDFNY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 120 ALKINYHPASEKVQA-LDEKIL-LIRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY QVLRFQD-EKA-LNVQDKKKIFSVLDLKG 147 KYISYDSSDKDDFSFAQKKEGYLAVAMNG h 7.4%; Similarity 28.1%; 25; Conservative Score 118; DB 1; Lo Pred. No. 3.33e+00; 26; Mismatches 31; Indels 7; Gaps 96

Search completed: Tue Job time: 12 secs. Sep 26 16:15:11 2000 S

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# ALIGNMENTS

TMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRNR 260

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TOMB J. F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHHANN R.D., KETCHM K.A., KLENK H.-P., GILL S., DOUGHERTY B NELSON K., OUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., KOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., HICKEY E.K., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J., COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WANTHEE L., WALLI COTTON M.D., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           025166
025166;
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01-JAN-1998 (TrembLrel. 05, Last sequence update)
01-NOV-1998 (TrembLrel. 08, Last annotation update)
PUTATIVE NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ HOMOLOG (HPAA).
                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter Bacteria; Proteobacteria; epsilon s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL; AE001526; AAD06549.1; -.
SEQUENCE 249 AA; 28513 MW; A3729951 CRC32;
                                                                                                                                                                                                                                       STRAIN-26695
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VALKLNYHPASEKVOALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILONQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 14.7%;
Similarity 25.1%;
57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 235; DB 2; Length 249;
Pred. No. 2.97e-19;
75; Mismatches 73; Indels
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Last sequence
Last annotation
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                                                                                                                                                                                                                                                                                                                                   r pylori).
subdivision; Helicobacter
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                               WALLIN
                                                                                                                                                                                                                                                                                                                                   group;
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RESULT

ID Q9ZLY2 PRELLMING.....

AC Q9ZLY2;

PT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last seque.

DT 01-MAY-1999 (TrEMBLrel. 10, Last annot

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Best Local
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Best Local :
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                                                                                                                                                                                                                                      "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 39:116-180(1999)
EMBL; AE001479; AAD06033.1; -.
                                                                                                                                                                                                                                                                                                     ALM R.A., LING L.-S.L., MOIR D.T., SMITH D.R., NOONAN B., GUILD B.C., TUMMINO P.J., CARUSO A., URIA-NICKE GIBSON R., MERBERG D., MILLS S.D.,
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori J99. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 99120557.
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-J99;
                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence
                                                                                                                         210 V-KGTDNSND-AIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
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                         VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
                                                     KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                          ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY
                                                                              QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKNNL--K-DPN---SPNLDTL--
YLIPAGFIKYTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLYSTMYKGT-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGL 151
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                                                                                                                                                                                                                        AE001479; AAD06033.1; -.
NCE 282 AA; 32075 MW;
                                                                                                                                                                11.0%;
Similarity 25.1%;
56; Conserva+**~
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Similarity 25.08;
58; Conservative
                                                                                                                                                                                                                                                                                                  , MOIR D.T., KING B.L., BROWN E.D.,
GUILD B.C., DEJONGE B.L., CARMEL G.
.., URIA-NICKELSEN M., MILLS D.M., IV
MILLS S.D., JIANG Q., TAYLOR D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  epsilon
                                                                                                                                                                Score 176; DB 2;
Pred. No. 3.63e-10;
59; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
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Pred. No. 5.53e-18;
75; Mismatches 76
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                                                                                                                                                                                                                         E982253F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282
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                                                                                                                                                                                           Length 282;
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  214
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KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG

- NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG

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01-JAN-1998
01-NOV-1998
SEQUENCE FROM N.A.

ALONSO J.C., LUDER G., STIEGE A.C., CHAI S., W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
EMBL; X97918; CAA66554.1; -.

SEQUENCE 179 AA; 20956 MW; 85120A6C CRC32;
                                                                                                                                                                                                                                                                         048453;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOMB J.F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E. HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                           Bacteriophage SPP1.
                                                                                                                                                                                                                                                        COMPLETE NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 278 AA; 31947 MW; 79127867 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 388:539-547(1997).
EMBL; AE000564; AAD07568.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-JAN-1998 (TrEMBLrel. 05, Created)
Ol-JAN-1998 (TrEMBLrel. 05, Last sequence update)
Ol-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 31.9 KD PROTEIN.
                                                                                                                                                                       Lambda phage group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; HP0492; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VENTER J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97394467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDQSSGSVWENFYEPESNRVVHDFAVEVGTFQAM-TY-TYKHN-NSGGLNSSNSIIHEYL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-NSNDAIKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLRFQD-EKA-LNAQDKRKIFSVLDLKGWVGILEDLKMNL--K-DPN---NPNLDTL-- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKNKEDAIHKILNRMYAVVMKKAVTELTKENIDKYREAIDRMKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGL-VS-TMVKG-T 213
                                                                                                                                                                                              dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 166; DB 2;
Pred. No. 1.05e-08;
62; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                          179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                      WEISE F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
                                                                                TRAUTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT
AC OSS
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                                                                                                    Query Match
Best Local s
Matches 2
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Best Local S
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O97281
O97281;
O97281;
O1-MAY-1999 (TEMBLrel. 10, 0
01-MAY-1999 (TEMBLrel. 10, 1
01-NOV-1999 (TEMBLrel. 12, 1
                                                                                                                                                                                                      CHARRON R.L., BARRY J.J., BU
Submitted (APR-1997) to the
EMBL; U97042; AAB581611; --
PFAM; PF00873; ACR_tran; 1.
PRINTS; PR00702; ACRIFLAVING
SEQUENCE 1027 AA; 110930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              006471;
006471;
01-JUL-1997
01-JUL-1997
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K61-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLITER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., B Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL, AL034559; CAB39027.1; -
SEQUENCE 578 AA; 68384 MW; 1AC1C75C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFC0895W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFC0895W PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                    405
     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EYEKYKKKMKEKSMEMDMDNE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EKTNSLEETLYQINNEYNKCIDMIEKEIHDNIDDKESLKYKNELEKL-C-VIKKEKDEKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 SIDSTUMDISELDIQEKTIKITHSSHSGGIVSTMVKGTDNSNDAIKRALNKIFANIMQEI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 DKK-LTQKNLESYQKDAKELKGKRN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 EEKELVLRGMEQY-KEIKKIREEMN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%;
Local Similarity 24.7%;
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 SLDDIGQALSDMDIDEAFNQAFQALDNSGFFKRAVRAYWKKNDSIIKALESQ-AKTIEDV 146
                       IGIVVDDAIVVVENVERNIENGMNARQATYKA-MQEVSGPIIAIALTLVAVFVPLAFMSG 463
LAVAMNGEIVLRPDPKRTIQK-KSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMS-GES 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFS-FAQK-KEGYLAVAMNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKYQALDEKILLLRPAFQ-YSDNIAKEYENKFKNQTALKVEQILQNQGYKVISVDSSDKD
                                                                                                 h 7.3%;
Similarity 15.2%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TremBirel. 04, (TremBirel. 04, (TremBirel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                      ACRIFLAVINRP.
AA; 110930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.7%;
                                                                                                                                                                                                                                                                                   to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                           BURNS J.L.;
1e EMBL/GenBank/DDBJ databases
                                                                                                 Score 116; DB 2; Le Pred. No. 6.05e-02; 62; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117; DB 5; Le
Pred. No. 4.55e-02;
22; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 6.35e-05;
27; Mismatches 31
                                                                                                                                                                                                      7C8108F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1027 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderia
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                                                                                                                                                    Length 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 578,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                 Gaps
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071192
071192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTLORE B., O'CALLAGHAN M.,
PARSONS J., PECY C., RIKKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
TELEBRAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             002080
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SIMILAR TO CCAAT/ENHANCER-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAMSLEY P., KRAMER J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Rhabditina; Rhabditoidea; Rhab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C48E7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94150718
                                                                                                                               199 SSHSGGLVSTMVKGTDNSND-AIKRAL-NKIFANIMQEIDKKL 239
                                                                                                                                                                                                                                          140 KSEPGL-LFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTH 198
                                                                                                                                                                                   157 LGELTVLMSKMMKGESITVEPSVKRALKHRVFIEKMKPVEDKM 199
                                                                                                                                                                                                                                                                          100 MTETEQEAFADLVAELETQTAEAVKAFSKVFDRME-EINDD-KEGLSLLKIKN-YEMTAY 156 ::| |: | | | | | | : : : :|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 7.1%;
Local Similarity 24.5%;
hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 LTGQFYKQFA-MTIAISTVISAFNSLTLSPALSAILLKGHGDKEDWLTRVMNRVLGGFFR 522
                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                      43 NDTAEKYDELKKENETLERKYEQLQKE-LSFL--KEMFMAYAKNDGNDGPPPPPPPSSSA 99
                                                                                                                                                                                                                                                                                                                                                     NOTALKYEQILQNQGYKVISYDSSDKDDFSFAQKKEGYLAVAMN-GEIVLRPDPKRTIQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDS-FTMDLSELDIQ-EKFLKTTHS-SHSGGLVSTMVKGTDNSNDAIKRALNKIFANIMQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFNKVF-HRGAENYGRGVRGVLSRK 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIDKKLTQKNLESYQKDAKELKGKR 258
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 114; DB 5; Le Pred. No. 1.07e-01; 42; Mismatches 71;
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                            549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHOWNKEEN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%;
Best Local Similarity 24.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.8%;
Best Local Similarity 24.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O85168 PRELIMINARY;
O85168;
01-NOV-1998 (TIEMBLITE1. 0
01-NOV-1998 (TIEMBLITE1. 0
01-NOV-1999 (TIEMBLITE1. 1
                                                   4377 IRGRLIRMAEDHHVLLLTLHHIVSDGWSVDVLTRELSALYAAFSQDQDDPLAPLELQ-Y 4434
                                                                                                                                                                                                                              4322 MOGDDGQPVQRISPADTGFNLQMHDLQG-LADAE-EKLQAL-A-SEESLQSFDLQGGPL- 4376
:: | : | : | : | : | | | | : | | | | : : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUENZI E., GRANDI G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF047828; AAC80285.1;
PROSITE; PS00455; AMP_BINDING; 8.
PFAM; PF005501; AMP-binding; 8.
PFAM; PF00550; pDUF4; 9.
PFAM; PF00550; pP-binding; 9.
PFAM; PF00975; Thioesterase; 1.
PRINTS; PR00154; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of the 3'-terminal two-thirds of the grapevine leafroll-associated virus-3 genome reveals a typical monopartite closterovirus-"; 1299-1307(1998).

EMBL; AF037268; AAC40708.1; -
SEQUENCE 549 AA; 59013 MW; 2B128E62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-NY1;
MEDLINE; 98264508.
MEDLINE K.-S., ZHU H.-Y., DRONG R.F., SLIGHTOM J.L., MCFERSON GONSALVES D.;
189 IQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKRALNKIFANIMQEIDKKLTQKNLESY 247
                                                                                                                                                                           129 LRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSELD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYRINGOMYCIN SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        grapevine leafroll-associated virus 3. Viruses; ssRNA positive-strand viruses, Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.AUG-1998 (TrEMBLrel. 07, Created)
01.AUG-1998 (TrEMBLrel. 07, Last sequence update)
01.AUV-1998 (TrEMBLrel. 08, Last annotation updat
59 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GFIKVTIL-E-PMSGESLDSFTMDLSELDIQEKFLKTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 DSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 DPVETDVAQFNLSTDGTVSVIVNGEEV-KNEYLVFGTTNVLDSLVYKSGREDLEAKAIPE 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 YLTTLNILHDKAFTRRNLGNKDKGFSDLRIEENFLKSA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9376 AA; 1029826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08,
12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            Score 107; DB 2; Length 9376; Pred. No. 7.37e-01; 33; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 14;
Pred. No. 4.27e-01;
30; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E4B2CD95 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 3;
                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.R.,
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                            6
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RESULT 12 ID 093582 AC 093582;

PRELIMINARY;

PRT;

387 AA

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q44769;
Q1-NOV-1996 (TremBLrel. 01, Created)
Q1-NOV-1998 (TremBLrel. 08, Last sequence update)
Q1-NOV-1999 (TremBLrel. 12, Last annotation updat
Transferrar PROTEIN (FLBC) (ORF20).
                                                                                                                                                                                                                                                                                                                                                                                   FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN
DOUGHERRY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALLBERG S., HANSON M.
YAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
                   SEQUENCE FROM N.A.

CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.
VAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTLACH P., BOWMAN C.,
UTTERBACK T., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
SUDMITTED (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q44769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00046; homeobox; 1.
Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 387 AA; 41738 MW; C862A1E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR EMBL; AF092538; AAC61772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAKAHASHI M., TAMURA K., BUSCHER D., MASUYA H., YONEI-TAMURA MATSUMOTO K., NAITOH-MATSUO M., TAKEUCHI J., OGURA K., SHIROJ OGURA T., IZPISHUA BELMONTE J.C., STORDING T., IZPISHUA BELMONTE J.C., Strong's luxoid (1stD), a 16 base pair deletion in the homeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
PAIRED TYPE HOMEODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alx-4.
Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                              Nature 390:580-586(1997).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
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                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tecal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKRALNKIFANI-MQEID 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPSGMDSSYLSVKEAGVKVPQDRASTDLPSPMDKADSESNKGKKRRNRTTFTSYQLEELE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKLTQKNL-ESYQKDAKELK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVFQKTHYPDVYAREQLAMR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.68;
Similarity 25.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98065943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08, Created)
08, Last sequence update)
12, Last annotation update)
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Pred. No. 1.26e+00;
20; Mismatches 38
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Best Local (
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Submitted (DEC-1995) to the EMBI
EMBL; AE001137; AAC66663.1; -
EMBL; U43739; AAA85608.1; -
HSSP; P13466; 1KSR.
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Q94895;
Q94895;
01-FEB-1997 (
01-FEB-1997 (
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YOLK PROTEIN:
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077338;
01-NOV-1998
01-NOV-1999
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DUNN J.J., E
                                                                                                                                                                                                                                                                                                                  HAMLIN N., LAWSON D., BARRELL B.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL008970; CAA15593.1; •
Eukaryota;
           Drosophila mimica (Fruit fly)
                                                                                                                                                                                                                     106
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                         -IKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDNSNDAIKR
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                                                                                                                                                                                                                  KDDFSFAQKKEGYLAVAMNGE-IVLRPDPKRTIQ-KKSEPGLLFSTGLDKMEGVLIPAGF
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Similarity 19.8%;
25; Conservative
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Alveolata; /
                                         7 (TremBirel. 02, 7 (TremBirel. 02, 8) (TremBirel. 08,
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Grembirel.
Grembirel.
Metazoa;
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                                1 (FRAGMENT).
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 Arthropoda;
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Pred. No. 1.26e+00;
43; Mismatches 53
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Pred. No. 9.65e-01
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           (Idiomyia mimica).
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Hexapoda;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp Run on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Sep 26 16:16:34 2000; MasPar time 23.61 Seconds 684.174 Million cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-09-308-435-2 (28-260) from US09308435.pep 1594 1 CSPHIIETNEVALKLNYHPA......CKNLESYQKDAKELKGKRNR 233

Searched: PAM 150 Gap 11 225878 seqs, 69334122 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 46.291; Variance 102.838; scale 0.450

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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INVASIN.	CELLOBIOSE DEHYDROGENA	ENDO-1,4-BETA GLUCANAS	SIMILAR TO CCAAT/ENHAN	FTSA.	CHROMOSOME X READING F	CEOB.	SUGAR TRANSPORTER.	FLAGELLAR PROTEIN (FLB	Y18D10A.11 PROTEIN.	PFC0565W PROTEIN.	59 KDA PROTEIN.	PFC0895W PROTEIN.	COMPLETE NUCLEOTIDE SE	HYPOTHETICAL 31.9 KD P	PUTATIVE PARALOG OF HP	PUTATIVE NEURAMINYLLAC	PUTATIVE PARALOG OF HP	THOUGHT THE THEORY OF DIND	NEITRAMTNYT.T.ACTOCE-BIND	Description	
2.78e+00 2.78e+00	2.14e+00	1.64e+00	1.64e+00	2.14e+00	1.26e+00	9.60e-01	9.60e-01	9.60e-01	1.26e+00	4.25e-01	4.25e-01	4.54e-02	2.97e-04	5.54e-08	1.99e-09	3.51e-17	1.92e-18	0.396.203	. :	Pred. No.	

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R11D1.10 PROTEIN. CELLOBIOSE DEHYDROGENA	,IPOPROTE	≫	MATURASE K (FRAGMENT).	z	FH1/FH2 PROTEIN HOMOLO	ATAXIN-2.	DEVELOPMENTAL REGULATO		PUTATIVE DNA RECOMBINA	ш	LIKE PR	YOLK PROTEIN 1 (FRAGME	H	PUTATIVE VOLTAGE-AND C		SENSORY TRANSDUCTION R	YVGQ PROTEIN.	TNIA PROTEIN.	FUNCTION UNKNOWN.	L3 RIBOSOMAL PROTEIN.	INIA.	TRANSPOSASE TNIA.		
	1.30e+01							1.01e+01	7.82e+00		6.05e+00		3.61e+00		•	3.61e+00	•	3.61e+00	3.61e+00	4.68e+00	2.78e+00	2.78e+00	٠	3

## ALIGNMENTS

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208 TMVKGTDNSNDAIKSALNKIFASINQENDKKLTQRNLESYQKDAKELKNKRNR 260	148 STGLDKMEGYLIPAGFYKYTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS 207 	88 EEILQNGGYKVINVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF 147  :	28 CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTTLKV 87 	Query Match 98.1%; Score 1564; DB 2; Length 260; Best Local Similarity 96.6%; Pred. No. 8.59e-263; Matches 225; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	"Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 39:176-180(1999). EMBL: AE001504; AAD06306.1; SEQUENCE 260 AA; 29199 MW; 9C0103A4 CRC32;	WEDLINE; 99120557.  ALM R.A., LING LS.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,  SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.,  TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C.,  GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,  TRUST T.J.;	Helicobacter pylori J99. Helicobacter pylori J99. Heacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter. [1] [1] [2] [3] [5] [5] [5] [5] [5] [6] [7] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8	OPZL47 PRELIMINARY; PRT; 260 AA.  OPZL47; PREMBLEL 10, Created)  O1-MAY-1999 (TIEMBLEL 10, Last sequence update)  O1-MAY-1999 (TIEMBLEL 10, Last sanotation update)  O1-MAY-1999 (TIEMBLEL 10, Last sequence Nodate)  REVRANTINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR.

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Matches
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Best Local
TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERRY B. NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.I. COTTON M.D., WEIDMAN J.M., FUJII C., BONMAN C., WATTHEY L., WALLI'L COTTON M.D., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PUTATIVE NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ HO
HP0410.
                                                                                                                                                                                             MEDLINE; 97394467.
                                                                                                                                                                                                                    STRAIN-26695;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; epsilon subdivision;
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                                                                                                                                                                                                                                                                                  Helicobacter.
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Nature 397:176-180(1999).
EMBL; AE001526; AAD06549.1; -.
SEQUENCE 249 AA; 28513 MW; A3729951 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUDMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.
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01-MAY-1999 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
PUTATIVE PARALOG OF HPAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SV-S-QFKDVSEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E-EKVID 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VELHFHY-PIKGKQEPKNNHLVVLIDPKIEANKVIPENYQKEFEKSLFLQLSNFLERKGY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 14.4%;
Similarity 25.1%;
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 230; DB 2; Le
Pred. No. 1.92e-18;
74; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Best Local (
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Best Local S
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Nature 388:539-547(1997).
EMBL; AE000557; AAD07478.1; -
TIGR; HP0410; -
Hypothetical protein.
SEQUENCE 249 AA; 28349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ZLY2
Q9ZLY2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOI SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOV
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001479; AAD06033.1; -. SEQUENCE 282 AA; 32075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic-sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-J99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
PUTATIVE PARALOG OF HPAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 99120557.
                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori J99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JHP0444.
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The complete genome sequence
                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 V-KGTDNSND-AIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKGKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 VHRIKETDHDQAIRKIMNQAYHKVMVHITKELSKKHMEHYEKVSSEMK-KRK
                                                                                                                                                                                                                  39
                                                                                                                                                                                                                                 152 DKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                        Local
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                                            VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD
VLIPAGFIKVTILEPMSGESLDSFTMDLSELD-IQEKFLKTTHSSHSGGLVSTMVKGT-D
                                                                                                 KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                                           QVLRFQD-EKA-LNVQDKKKIFSVLDLKGWVGILEDLKNNL--K-DPN---SPNLDTL---
                                                                                                                                                                                                  ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKVID-M-SSGYLNLNFVEPKSEDIIHSFGIDVSKIKAVIER-VEL-RRTNSGGFVPKTF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERKGYSV-S-QFKDASEIPQDIKEKALLVLRMDGNVAI-LE-D-IVEE-SDA--L-S-E- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETNE-VALKLNYHPASEKVQALDEK-ILLLRPAFQYSDNIAKEYENKFKNQTALKVEQIL
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                                                                                                                                                                                                                                                                                                              h 10.7%;
Similarity 25.1%;
56; Conservative
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Similarity 25.0%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria;
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                                                                                                                                                                                                                                                                                                        Score 171; DB 2; Le
Pred. No. 1.99e-09;
58; Mismatches 91;
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Last annotation updat
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Pred. No. 3.51e-17;
74; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            E982253F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>:</del>:
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                                                                                                                                                                                                                                                                                                        Indels 18;
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                                                                                                                                                                                                                                                                                                      Gaps
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Matches 5
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SEQUENCE FROM N.A.
ALONSO J.C., LUDER G., STII
Submitted (MAY-1996) to the
EMBL; X9791B; CAA66554.1; -
SEQUENCE 179 AA; 20956 b
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Nature 388:539-547(1997).
EMBL; AE000564; AAD07568.1;
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TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A. FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A. NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., NELOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOMMAN C., WAITHEY L., WALLIN E HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M., VENTER B.
                                                                                                     Bacteriophage SPP1.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 278 AA; 31947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                     COMPLETE NUCLEOTIDE SEQUENCE.
                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                  048453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; HP0492; -.
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                 048453;
                                                                                          Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                       214 D-NSNDAIKSALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                                                                                                                                                                                                                                                                                                     157
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                                                                                                                                                                                                                                                                                                                                                    VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAM-TY-TYKHN-NSGGLNSSNSIIHEYL
                                                                                                                                                                                                                                                                                                                                                                                                                   QVLRFQD-EKA-LNAQDKRKIFSVLDLKGWVGILEDLKMNL--K-DPN---NPNLDTL-- 168
                                                                                                                                                                                                                                                                                                                                                                                             KVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
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                                                                                                                                                                                                                                                                                                      EKNKEDAIHKILNRMYAVVMKKAVTELTKENIDKYREAIDRMKG 269
                                                                                                                                                                                                                                                                                                                                     VLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGL-VS-TMVKG-T
                                                                                          phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 56; Conser
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%;
larity 25.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                        group
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   20956
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                                             STIEGE A.C.,
                             the
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   WW.
                                                                                                        RNA
                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 161; DB 2;
Pred. No. 5.54e-08;
61; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                               EMBL/GenBank/DDBJ
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                                                                                                      stage;
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   85120A6C
                                             CHAI
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   CRC32
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                                                                                                     phages;
                                             WEISE
                                databases
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                                             'EJ
                                                                                                      Siphoviridae
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                                             TRAUTNER
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RESULT
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Query Match
Best Local S
Matches 2
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Best Local S
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                      "Nucleotide sequence of the 3'-terminal two-thirds leafroll-associated virus-3 genome reveals a typica closterovirus.";
J. Gen. Virol. 79:1299-1307(1998).
EMBL; AF037268; AAC40708.1;
SEQUENCE 549 AA; 59013 MW; 2B128E62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   071192
071192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIVER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., B Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL034559; CAB3907.1; -. SEQUENCE 578 AA; 68384 MW; 1AC1C75C CRC32;
                                                                                                                                                                                                                           LING K.-S., ZHU H.-Y., DRONG R.F., GONSALVES D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                              STRAIN-NY1
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       grapevine leafroll-associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                Closterovirus.
                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                59 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium
                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-3D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFC0895W PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 7.3%;
Local Similarity 24.7%;
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFS-FAQK-KEGYLAVAMNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYEKYKKKMKEKSMEMDMDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKVQALDEKILLLRPAFQ-YSDNIAKEYENKFKNQTALKVEQILQNQGYKVISVDSSDKD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTNSLEETLVQINNEYNKCIDMIEKEIHDNIDDKESLKVKNELEKL-C-VIKKEKDEKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKK-LTQKNLESYQKDAKELKGKRN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEKELVLRGMEOY-KEIKKIREEMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLDDIGQALSDMDIDEAFNQAFQALDNSGFFKRAVRAYWKKNDSIIKALESQ-AKTIEDV 146
  Similarity
24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 8.4%;
Similarity 28.2%;
24; Conservative
                                                                                                                                                                                                                                                                       98264508.
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6.8%;
larity 24.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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08,
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Last sequence up
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Pred. No. 2.9
26; Mismatcl
Score 109; DB 14;
Pred. No. 4.25e-01;
30; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
22; 1
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
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                                                                                                                                                                                                                                                SLIGHTOM
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                                                                                                                                                                                                                                                                                                                                                                                  no DNA stage;
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                                                                                                                                                                                                                                           J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                             typical
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                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium.
                                                                                                                                                                                                                                                MCFERSON J.R.,
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578;
                                                                                                                                                                                                  the grapevine
                                                                                                                                                                                                                                                                                                                                                                                  Closteroviridae;
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                                             549;
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DPVETDVAQFNLSTDGTVSVIVNGEEV-KNEYLVPGTTNVLDSLVYKSGREDLEAKAIPE 502

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SEQUENCE FAVOR ....
MEDLINE; 94150718.
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
WILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GAEDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           est Local
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TREMBLREL. 1
01-NOV-1999 (TREMBLREL. 1
Y18D10A.11 PROTEIN.
Y18D10A.11
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01-NOV-1998 (Trem
01-NOV-1999 (Trem
PFC0565W PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
HARRIS B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            "2.2 Mb of contiguous nucleotide sequence
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9XW20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMLIN N., LAWSON D., BARRELL B.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL008970; CAA15593.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-3D7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 -IKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMYKGTDNSNDAIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 KDDFSFAQKKEGYLAVAMNGE-IVLRPDPKRTIQ-KKSEPGLLFSTGLDKMEGVLIPAGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703 NEDLLFDENNRYYTNIRKSDICIYIKEIKNNNINLNKVDKKMIFYLLKEKKNIIFIVNKI 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 6.8%;
Local Similarity 19.8%;
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLNLF 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLILTNFEKKRNDFLQEFS-NLFN-DIPIIFLNTKNNTHINTLLNKIIHIHKMNNVIIST 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALNKIF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLTTLNILHDKAFTRRNLGNKDKGFSDLRIEENFLKSA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFIKVTIL-E-PMSGESLDSFTMDLSELDIQEKFLKTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TremBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                   N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       pda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 5; Le
Pred. No. 4.25e-01;
44; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5043B736 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                                                                                                              얁
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AC CONTRACTOR REPORTED TO THE PROPERTY OF STREET ST
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Best Local S
Matches 2
Query Match
Best Local
                                                                                                                                                                         DUNN J.J., BUTLER-LOFFREDO L., Submitted (DEC-1995) to the EMEMBL; AE0001137; AAAC66663.1; -- EMBL; U43739; AAA85608.1; -- HSSP; P13466; 1KSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHICRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALLBERG S., HANSON M.,
VAN-YUGT R., PALMER N., DAMS M.D., GOCAYNE J.D., WELDMAN J.,
UTIERBACK T., WAITHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHICRA R., WHITE O., KETCHUM K.A., DODSON R.C., HICKEY E.K., GWINN M
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
VAN-YUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,
UTTERBACK T., WAITHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
burddorferi.":
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 98065943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
8661-VON-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q44769;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans.";
nature 368:32-38(1994).
EMBL; AL034393; CAA22314.1; -.
SEQUENCE 248 AA; 27963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLAGELLAR PROTEIN (FLBC) (ORF20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q44769
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3-394 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 MSGE-SIDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTDN-SNDA-IKSALNKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ANIMQEI 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 QDAEVSMTTLKETVAKLEEENNVLQATWAEERSGLVNELIDTKEKLAKSAQAQTELDESH 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 RDIMTAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 QKRWEGELASSRAQNEQL-SEEKSQLQKENE-ELLLVL-L-RTEGIVDANKSLSEQLANA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKK-EGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEP
                                                                                       394
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(TrEMBLrel. 08, Last sequence up
(TrEMBLrel. 12, Last annotation
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ilarity 22.0%;
Conservative
                                                                                    AA;
                                                                                    45073 MW;
Score 106; DB 2;
Pred. No. 9.60e-01
                                                                                                                                                                                                                                                        .., KIELECZAWA J.,
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105; DB 5; L
Pred. No. 1.26e+00;
40; Mismatches 51;
                                                                                 5BF8FA60 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC3B5F9C CRC32;
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                                                                                                                                                                                                                                                           MEDALLE J., databases.
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                                                                                                                                                                                                                                                                                         LUFT
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Similarity

6.6%; 19.7%;

Length 394;

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                      KEMNER J.M., LIANG X., NESTER J. Bacteriol. 179:0-0(0).
EMBL; U91632; AAB51510.1; -.
PFAM; PF00005; ABC_tran; 2.
Sugar transport.
SEQUENCE 512 AA; 56512 MW;
                                                                                                                                                    006471
006471;
006471;
01-JUL-1997
01-JUL-1997
01-NOV-1999
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01-JUL-1997
01-NOV-1998
                  STRAIN-K61-3;
CHARRON R.L., BARRY J.J., BUR
Submitted (APR-1997) to the E
EMBL; U97042; AAB58161.1; -.
PPAM; PF00873; ACR_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UT 12
005176
                                                                                                 Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens. Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobiaceae;
                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365
                                                                                                                                                                                                                                             215
                                                                                                                                                                                                                                                       411 GGNQQ-KVVLSKWLFSN 426
                                                                                                                                                                                                                                                                                                           353 LGLVLNDNILHNTTLANLAGVSKASIIDDIKEMKVASDF-RTRLRIRSSGIFQETVN-LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                      295 IAGLMGAGRTEFAMSVFGKSY-GHRITGDVLIDGKPVDVSTVRKAIDAGLAYVTE-DRKH 352
                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                       6.6%;
Local Similarity 21.2%;
les 29; Conservation
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                                                                                                                                                                                                                                                                                     -GVLIPAGFIKVTILEPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVSTMVKGTD
 PR00702;
E 1027 A
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                                                                                                                                                     (TrEMBLrel. 04,
(TrEMBLrel. 04,
(TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                  PRELIMINARY;
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ACRIFLAVINRP.
A; 110930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          56512 MW;
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                                          BURNS J.L.;
ne EMBL/GenBank/DDBJ
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Last sequ
Last anno
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Pred. No. 9.60e-01;
45; Mismatches 54;
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                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          C6F6AEAC CRC32;
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 7C8108F2
                                                                                                                                                                                                  1027
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                                                                                                          Burkholderia group;
                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae
                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                  Length
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Best Local Similarity 25.6%;
Matches 21; Conservative
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Best Local Similarity 14.5%;
Matches 21; Conservative
STRAIN=212;
MEDLINE; 97234641.
GE Y., OLD I.G., SAINT GIRONS I., CHARON N.
GE Y., OLD I.G., SAINT GIRONS I., CHARON N.
"Molecular characterization of a large Borr
operon which is initiated by a consensus si
J. Bacteriol. 179:2289-2299(1997).
EMBL; L76303; AABS1416.1; -.
HSSP; P13466; 1KSR.
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Q44919
Q44919;
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01-NOV-1996
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Submitted
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P87192; O1-JUL-1997 (TrEMBLrel. 04, Created)

O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)

O1-JUL-1997 (TrEMBLrel. 04, Last annotation update)

CHROMOSOME X READING FRAME ORF YJL114W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases EMBL; Z49389; CAA89409.1; -.
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; (
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ZIEPLUCH C., KORDES
submitted (OCT-1995)
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Spirochaetaceae; Borrelia
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Last sequence update)
Last annotation update)
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Pred. No. 1.26e+00;
28; Mismatches 29
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Pred. No. 9.60e-01
62; Mismatches 5
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SEQUENCE 394 AA; 45005 MW; 57F04C42 CRC32;

Query Match
3est Local Similarity 20.9%; Pred. No. 2.14e+00;

4atches 24; Conservative 40; Mismatches 45; Indels 6; Gaps 6;

249 DFVSSLKPEWNLKINKNIVDKA-KVV-LKSNNTGEIKLVLKPKELGSIRINLNLDSNNNL 306
::::| | | | | ::::| | | | | :::|
74 EYENKFKNQTALKVEQILQNQGYKVISVDSSDKDDFSFAQK-KE-GYLAVAMNGEIVLRP 131

307 LGKIVVDNQNYK-MLFDQNMHSINKMLGESGF-NASLNLFLAGENLNSFTGDFKD 359
| | ::::| | | | | | :::| | | | | | | ::|
132 DFKRTIQKKSEPGLLFSTGLDKMEGVLIPAGFIKVTILEPMSGESLDSFTMDLSE 186

Arch completed: Tue Sep 26 16:17:02 2000
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(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: .Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Sep 26 16:18:57 2000; MasPar time 8.99 Seconds 613.770 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence:

>US-09-308-435-4
(28-260) from US09308435.pep
1599
1 CSPHIIETNEVALKLNYHPA......QKNLESYQKDAKELKGKRNR 233

Searched: PAM 150 Gap 11

Scoring table:

188963 seqs, 23686106 residues

Database: Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq36 1:geneseqp

Statistics: Mean 32.470; Variance 175.985; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

17 18 20 21 23	112 12 14 15	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No. 1 2
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nit of yea size origius paragalus paragalus paragalapical-endapica	C Seco	pylori olerae t ilap20 rived pr rived pr rived pr rived pr f 01ae11	Description Helicobacter pylori su Helicobacter pylori 29 Helicobacter pylori 29
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•	

## ALIGNMENTS

CC (T4383); a sequence (W07549) deduced from a second cDNA clone CC (T43834) differs only at position 222 (Ser for Arg). Recombinant CC antigen can be produced in transformed host cells. It is useful CC for the diagnosis and treatment of H. pylori infections and for CC use as a vaccine.  SQ sequence 250 AA;  Query Match  100.0%; Score 1599; DB 1; Length 260;  Best Local Similarity 100.0%; pred. No. 2.57e-113;
protein
therapy; diagnosis. Helicobacter pylori strain CCUG 17874 (NTCC 11637). Key Location/Qualifiers peptide 1. 27 /label= Sig_peptide cleavage_site 25. 28
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RESULT
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                                                                                                                                                                                                                                                                                               ps Disclosure; Page 35-36; 5lpp; English.

This polypeptide comprises a 29 kDa surface antigen which is carpressed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is an adhesin that is conserved in all tested strains of H. pylori, and is also a putative virulence factor. The invention relates to negatively charged lipid or lipid mixture and at least one antigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see w34643) coding for such an antigen. The new formulations, which are useful as vaccine formulations, endict are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second, claimed 29 kDa antigen (see w60156) is provided that differs only at residue 222 (Ser for Arg).
                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 23
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28-MAY-1998.
18-NOV-1997; SE1927.
22-NOV-1996; SE-004296.
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Helicobacter pylori 29 kDa surface-exposed antigen.
Cell surface antigen; adhesin; infection; vaccine; drug delivery.
Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responses
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Local Similarity 100.0%;
les 233; Conservative
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TMVKGTDNSNDAIKRALNKIFANIMOEIDKKLTQKNLESYQKDAKELKGKRNR 260
                                                       CSPHIIETNEVALKLNYHPASEKVQALDEKILLLRPAFQYSDNIAKEYENKFKNQTALKV
                                                                                                                   POILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
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98-312174/27.
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0; Mismatches 0;
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Antigen; adhesin; immunogen; therapy; diagnosis. Helicobacter pylori strain C

diagnosis.
cter pylori strain CCUG 1787
Location/Qualifiers

17874

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/label= Sig\_peptide
25. .28

W07449; 04-MAR-1997 W07449

standard;

Protein;

260

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Helicobacter pylori

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypertide comprises a 29 kDa surface antigen which is expressed on the surface of both dividing (bacillary) and resting (colloid) forms of Helicobacter pylori. The antigen gives rise to both systemic and local (mucosal) production of antibodies. It is an adhesin that is conserved in all tested strains of H. pylori, and is also a putative virulence factor. The invention relates to a new pharmaceutical composition comprising a lipid aggregate of a negatively charged lipid or lipid mixture and at least one antigenic, native or recombinant antigen of H. pylori, preferably the surface-exposed 29 kDa antigen, or a nucleic acid (see v34642) coding for such an antigen. The new formulations, which are useful as vaccine formulations, elicit a protective immune response against H. pylori infections, and are suitable for therapeutic and prophylactic use. An adequate response is produced even without adjuvant. A second 29 kDa antigen (see W60157) is provided that Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local:
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Berglindh T, Lofroth J
WPI; 98-312174/27.
N-PSDB; V34642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1998 (first entry)
Helicobacter pylori 29 kDa surface-exposed antigen.
Cell surface antigen; adhesin; infection; vaccine; drug delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W60156 standard; Protein; 260
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22-NOV-1996;
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Similarity 99.6%;
232; Conservative
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SE-004296.
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Pred. No. 1.58e-11
0; Mismatches
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C A 29 kDa antigen (W07449) of Helicobacter pylori is an adhesin expressed on the surface of resting and dividing forms of the bacterium. It is conserved in all tested strains of H. pylori, and gives rise to both systemic and local (mucosal) prodn. of antibodies. Its amino acid sequence was deduced from a cDNA clone (T43834); a sequence (W07550) deduced from a second cDNA clone (T43835) differs only at position 222 (Arg for Ser). Recombinant antigen can be produced in transformed host cells. It is useful for the diagnosis and treatment of H. pylori infections and for series as a vaccine.
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Best Local (
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                                                                                                                                                                                                         26-NOV-1998.
21-MAY-1997;
21-MAY-1997;
                                                                                                                                                                                                                                                                                                  duodenal ulcer.
Chimeric - Helicobacter pylori.
Chimeric - Vibrio cholerae.
Fusion gene consisting of the Helicobacter pylori adhesin gene
ligated to the A2 and B subunit gene of Vibrio cholerae toxin
useful in the diagnosis and treatment of H. pylori
Claim 2; Page 20-21; 32pp; English.
                                                                                                                                  WPI; 98-434925/37.
                                                                                                                                                     21-MAY-1997; 000091.
21-MAY-1997; WO-KR0091.
(DAEW-) DAEWOONG PHARM CO
Kim BO, Lee BK, Park SK, Y
                                                                                                           N-PSDB; X21955.
                                                                                                                                                                                                                                                                                     W09853082-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          Fusion gene, H.
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Adhesin/V.cholerae toxin A2 and B
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18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 5
W74466 standard;
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Bolin I, Svennerholm A;
WPI; 97-034307/03.
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01-JUN-1995; SE-002007.
21-MAR-1996; SE-001085.
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                                                                                                                                                                                                                                                                                                                                                                                   subunit; B subunit;
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larity 99.6%;
Conservative
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peptidase
28. .260
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/note= "either the uncleaved or mature protein
be used in applns. of the invention"
                                                                                                                                                                                                                                                                                                                                                                                   infection;
diagnosis;
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Pred. No. 1.
0; Mismatc
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adhesin gene; V. cholerae toxin;
vaccine; gastritis; gastric ulce
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..58e-112;
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Best Local S
Matches 23
  infections (1) Page 207-208; 279pp; English.
Claims 27, 31; Page 207-208; 279pp; English.
Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life
                                                                                                                                                                                                                                                                                                                                                                                               Alm RA, Smith D;
WPI; 98-271811,224.
N-PSDB; X30467.
Helicobacter pylori nucleic acids and proteins -
products for the detection, prevention and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori ORF 11ap20714 4797137 f3_45
Vaccine; probe; diagnostic; ORF; cell
secreted protein; cellular protein.
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14-JUL-1997; US-891928.
28-OCT-1996; US-739150.
06-DEC-1996; US-759739.
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Pred. No. 1.58e-112;
0; Mismatches 1;
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                                                                                                                                                                                                                           Pf Helicobacter pylori nucleic acid sequences and related Pf polypeptide(s) - useful for vaccines to treat or prevent H. pylori Pf infection, and to detect Helicobacter Displosure; Page 1363-64; 1481pp; English.

CC This sequence represents a H. pylori protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds; CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified C1 solated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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Berglindh OT, Sm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
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STGLDKMERVLIPAGFVKVTILKPMSGESLDSFTMDLSELDIQEKFLKTTHSSHSGGLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
                                              EQILQNQGYKVISVDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLF
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                                                                                                                                                                       Conservative
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95.3%;
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                                                                                                                                                                    Score 1540; DB 1;
Pred. No. 1.14e-108;
7; Mismatches 4;
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life cycle; activator;
chronic gastritis;
                                                                                                                                                                      4
                                                                                                                                                                                                   Length 268;
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                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents an H. pylori derived protein, no further details are given in the specification.

C details are given in the specification.

C Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequences. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or or use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of pylori whole genomic DNA was isolated and nebulised to a median size of pylori-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Thesefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of sequenced.
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Best Local S
Matches 4
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W24663;
W24663;
12-AUG-1997
              29-JUL-1997 (first entry)

H. pylori derived protein.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duddenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                       W20454 standard; protein; W20454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T77481.

Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics claim 18; Page 178; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; cytoplasmic; cell envelope; flagella; transport secreted; periplasmic; chronic gastritis; duodenal ulcer disea activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition.
   Helicobacter
                                                                                                                                                                                                                                                                                                                                     Note: The ORF/protein reference number for this sequence was obtained from the related specification, W09640893.
Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1996; U18542.
17-NOV-1995; US-561469
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                                                                                                                                                                                      Local Similarity
les 43; Conse
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larity 97.7%;
Conservative
   pylori
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Pred. No. 5.
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                                                                                                                                                                                                                                                                               DB 1;
5.74e-13;
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Disclosure; Page 655; 1481pp; English.

The present sequence is a H. pylori derived protein, no further details are given in the specification.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from cverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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Best Local
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09-OCT-1997; U05223.

27-MAR-1997; U05-761318.

29-MAR-1996; US-625811.

02-APR-1996; US-758731.

25-OCT-1996; US-736905.

28-OCT-1996; US-738859.
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19-06-1996;
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
01-APR-1996; US-630405.
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection Claims 14,80; Page 653; 1145pp; English.

This sequence is a H. pylori cell envelope outer membrane protein (OMP) The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  W55445;
W55445;
                                                                                                                                                                (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastritis; di
                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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N-PSDB; T67801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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larity 97.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; I
.74e-13;
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A (ASTR ) ASTRA AB.

A (ASTR ) ASTRA AB.

PI Alm RA, Smith D;

RWP1; 97-503122/46.

PR Helicobacter pylori nucleic acid sequences and encoded prolypeptide(s) - useful in vaccines to treat or prevent H. pylori prolypeptide(s) - useful in vaccines to Infection

PT infection and for diagnosis of H. pylori infection

PT infection and for diagnosis of H. pylori infection.

CC This sequence is a H. pylori protein of unspecified function.

CC This sequence is a H. pylori protein of unspecified function.

CC The protein may be used in a vaccine to prevent or treat H. pylori

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors. The

CC UNA and probes derived from it may be used for the identification of

CC UNA and probes derived from it may be used for the identification. Nucleic
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Best Local
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                                                                                                                                                                                                                                                                           WO9737044-A1.
09-CCT-1997; U05223.
27-MAR-1996; US-761318.
29-MAR-1996; US-625811.
29-MAR-1996; US-758731.
25-CCT-1996; US-736905.
28-CCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1998 (first entry)
H. pylori ORF hp3el1075orf3 protein.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W55332;
15-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W55332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
57; Conser
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larity 25.1%;
Conservative
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are not given in the spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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Pred. No. 3.94e-08;
75; Mismatches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                               encoding this amino acid the specification"
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           Query Match
Best Local S
Matches 5
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01-APR-1998, U06371.

29-JUL-1997, US-902615.

01-APR-1997, US-833457.

24-JUN-1997, US-881227.
                                                                                                                                          New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 8; Page 455-456; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating the inventions, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for the production of antibodies. The products can also be used for the production of antibodies.
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Helicobacter pylori.
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W98332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; X14051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al-Garawi A, Kleanthous WPI; 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(INNR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9843478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ylori GHPO 1615 protein.
protein; Helicobacter infection;
ic ulcer disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLIPAGFIKVTILEPMSGESLDSFTMDLSEL-DIQEKFLKTTHSSHSGGLVS-TMV-KGT 213
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           Similarity
58; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AA;
   14.2%;
larity 25.0%;
Conservative
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larity 25.1%;
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PO 1615 protei
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Score 227; DB 1; Le
Pred. No. 1.46e-07;
75; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 235; DB 1;
Pred. No. 3.94e-08;
75; Mismatches 73
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WPI; 98-271811/24.
N-PSDB; X30418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori nucleic acids and proteins - products for the detection, prevention and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. Dylori OrF 04-0-11108_3906963_fl_7 cell envelope protein. Vaccine: probe; diagnostic; ORF; cell envelope protein;
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07-MAY-1998.
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Y10951 standard; Protein;
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                                                                                                                                                                                                                             KVISYDSSDKDDFSFAQKKEGYLAVAMNGEIVLRPDPKRTIQKKSEPGLLFSTGLDKMEG 156
                                                                                                                                                                                                                                                                                                                                                   ALKLNYHPASEKVQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96
- NSNDATKRALNKIFANIMQEIDKKLTQKNLESYQKDAKELKG
                                                    KNREDAIHKILNRMYAVVMKKAVTELTKENIAKYRDAIDRMKG
                                                                                                                                                                   VDQSSGSVWFNFYEPESNRVVHDFAVEVGTFQAITYTYTSTNNASGGFNSSKSVIHENLD 230
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Similarity 25:1%;
56; Conservation
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Pred. No. 5.19e-04;
59; Mismatches 90;
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The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
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06-JUN-1996;
07-JUN-1995;
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Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berglindh OT, Smi
WPI; 97-052306/05.
N-PSDB; T68191.
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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; binding cycle; activator; bacteria; life cycle; activator; binding cycle; life cycle; activator; binding cycle; life cycle; life
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                                                                                                                                   WO9640893-Al.
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Pred. No. 5.19e-04;
59; Mismatches 90;
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This sequence represents a H. Pylori secreted or periplasmic protein. CC The protein may be used in a vaccine to prevent or treat H. Pylori infection or to identify H. Pylori polypeptide binding compounds, cc useful as potential H. Pylori life cycle activators or inhibitors. CC The genomic sequence of H. Pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial CC DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To classify likely H. Pylori antipens for vaccine development, the amino CC identify likely H. Pylori antipens for vaccine development, the amino CC acid sequences predicted from various ORF were analysed for significant can't determined the sequences of interest, particular regions can be isolated from H. Pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASTR ) ASTRA
Berglindh OT,
WPI; 97-052306
                                                                                                                                                                                                                                                                                                                                                                      polypeptide(s) - useful for vaccines infection, and to detect Helicobacter Claim 72; Page 638; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid
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Length 147;
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or preve
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                                                Best Loc
Matches
64 PLDENY-PV-HIVQAPQNHHVVGILMPRIQVSDNL-KPYIDKFQDALINQIQTIFEKRGY 120
                                              7.4%;
Local Similarity 28.1%;
nes 25; Conservative
                                              Score 118; DB 1;
Pred. No. 3.41e+00;
26; Mismatches 31
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ALKLNYHPASEKYQA-LDEKIL-LLRPAFQYSDNIAKEYENKFKNQTALKVEQILQNQGY 96

Ş 닭 121 QVLRFQD-EKA-LNVQDKKKIFSVLDLKG 97 KVISVDSSDKDDFSFAQKKEGYLAVAMNG

8

39

Query Match

Search completed: Tue Job time: 12 secs. Sep 26 16:19:09 2000